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OM protein - protein search, using sw model

Run on: February 1, 2002, 09:56:24 ; Search time 24.48 Seconds

(without alignments)
502.831 Million cell updates/sec

Title: US-09-378-759-11_COPY_1_547

Sequence: 1 LLAVEETLMDSTATAELG.....IIGSSAGVLIAYVYIAI 547

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCPUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2895	100.0	970 2	US-08-449-645A-11 Sequence 11, Appl
2	2895	100.0	970 2	US-08-702-367A-11 Sequence 11, Appl
3	2895	100.0	970 5	PCT-US95-04681-11 Sequence 11, Appl
4	2870	99.1	994 4	US-08-542-635-2 Sequence 2, Appl
5	2785	96.2	995 1	US-08-162-809-18 Sequence 18, Appl
6	2785	96.2	1011 1	US-08-162-809-12 Sequence 12, Appl
7	2758	95.3	995 2	US-08-673-789-5 Sequence 5, Appl
8	2087.5	72.1	984 2	US-08-162-809-14 Sequence 6, Appl
9	1898.5	65.6	951 1	US-08-162-809-2 Sequence 2, Appl
10	1804	62.3	973 1	US-08-162-809-10 Sequence 10, Appl
11	1804	62.3	988 1	US-08-162-809-14 Sequence 14, Appl
12	1800.5	62.2	998 2	US-08-449-645A-20 Sequence 20, Appl
13	1800.5	62.2	998 2	US-08-449-645A-20 Sequence 20, Appl
14	1800.5	62.2	998 5	PCT-US95-04681-20 Sequence 20, Appl
15	1765.5	61.0	993 1	US-08-348-143-1 Sequence 20, Appl
16	1765.5	61.0	993 1	US-08-571-785-1 Sequence 1, Appl
17	1765.5	61.0	993 4	US-09-192-435-1 Sequence 1, Appl
18	1761.5	60.8	970 2	US-08-673-789-7 Sequence 7, Appl
19	1675.5	57.9	967 2	US-08-162-809-8 Sequence 8, Appl
20	1485.5	51.3	967 2	US-08-449-645A-30 Sequence 30, Appl
21	1485.5	51.3	967 2	US-08-702-367A-10 Sequence 30, Appl
22	1485.5	51.3	991 2	US-08-449-645A-13 Sequence 13, Appl
23	1485.5	51.3	991 2	US-08-702-367A-13 Sequence 13, Appl
24	1485.5	51.3	991 5	PCT-US95-04681-13 Sequence 13, Appl
25	1481	51.2	1005 2	US-08-469-537A-103 Sequence 103, Appl
26	1476.5	51.0	983 2	US-08-167-919A-10 Sequence 10, Appl
27	1476.5	51.0	983 2	US-08-449-645A-21 Sequence 21, Appl

28	1476.5	51.0	983 2	US-08-702-367A-21 Sequence 21, Appl
29	1476.5	51.0	983 3	US-08-715-106-10 Sequence 10, Appl
30	1476.5	51.0	983 5	PCT-US95-04681-21 Sequence 21, Appl
31	1474.5	50.9	983 1	US-08-162-809-16 Sequence 16, Appl
32	1472.5	50.9	986 2	US-08-673-789-3 Sequence 3, Appl
33	1468.5	50.7	986 2	US-08-449-645A-15 Sequence 15, Appl
34	1468.5	50.7	986 2	US-08-702-367A-15 Sequence 15, Appl
35	1468.5	50.7	986 5	PCT-US95-04681-15 Sequence 15, Appl
36	1466	50.6	982 2	US-08-673-789-4 Sequence 4, Appl
37	1461.5	50.5	1104 1	US-08-222-616-36 Sequence 36, Appl
38	1461.5	50.5	1104 5	PCT-US95-04228-36 Sequence 36, Appl
39	1455	50.3	998 2	US-08-449-645A-17 Sequence 17, Appl
40	1455	50.3	998 2	US-08-702-367A-17 Sequence 17, Appl
41	1455	50.3	998 5	PCT-US95-04681-17 Sequence 17, Appl
42	1453.5	50.2	993 4	US-08-368-776A-11 Sequence 11, Appl
43	1446	49.9	610 4	US-08-368-776A-3 Sequence 3, Appl
44	1446	49.9	610 5	PCT-US96-00419-3 Sequence 3, Appl
45	1446	49.9	626 4	US-08-368-776A-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-449-645A-11
Sequence 11, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-11

Query Match 100.0%; Score 2895; DB 2; Length 970;
Best Local Similarity 100.0%; Pred. No. 5.5e-246;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	LLAAVEETLMDSTATAELGVMVHPGSGMEVSCYDENMNTIRTYOVCNVESSQNMRLR	60
QY	61	TKFTRRGARRIHVEMKFSYRDCSSIPVSGCKETFNLYYEADPDSATKTPNNMNP	120
DB	61	TKFTRRGARRIHVEMKFSYRDCSSIPVSGCKETFNLYYEADPDSATKTPNNMNP	120
QY	121	VWKVDITADESFQVDLGGRVKMKINTEVRSFGPVRSRGTYLAFQDYGGMSLIAVRFY	180

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Db 121 WVKVDTIADESFQVDLGGVMMKINTEVRSFGVSRSGFTLAFQDYGCGMSLIVAVFY 180
QY 181 RKCPRILONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 240
Db 181 RKCPRILONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 240
QY 241 MCKAGFEAVENGTCVRCGCPSPGTFKANGDDEACTHCPINSRTTSEGAATNCVCRNGYTRADL 300
Db 241 MCKAGFEAVENGTCVRCGCPSPGTFKANGDDEACTHCPINSRTTSEGAATNCVCRNGYTRADL 300
QY 301 DPLMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSCSGRGACTR 360
Db 301 DPLMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSCSGRGACTR 360
QY 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDSPSPQFASVNIITNOA 420
Db 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDSPSPQFASVNIITNOA 420
QY 421 APSAVSIMHOVSTVDSITLSWSQDPQNGVILIDYELQYEEKELSEYNATAIKSPNTVT 480
Db 421 APSAVSIMHOVSTVDSITLSWSQDPQNGVILIDYELQYEEKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEYQTSIOEKPLIIGSSAAGLVFLI 540
Db 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEYQTSIOEKPLIIGSSAAGLVFLI 540
QY 541 AVVVIAT 547
Db 541 AVVVIAT 547

RESULT 2
US-08-702-367A-11
; Sequence 11, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702.367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-367A-11

Query Match 100.0%; Score 2895; DB 2; Length 970;
Best Local Similarity 100.0%; Pred. No. 5.5e-246;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 LLAAVEETIMDSTTATAEIGMWVHPSPGWESEYGYDENMNTIRTYQVCNVSESSQNNMLR 60
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Db 61 TKFIRRRGAHRIHVEKFIYSVRODCSSIPSVGSCKETFNLYYYEADPDSATKTFPMWMEHP 120
QY 121 WVKVDTIADESFQVDLGGVMMKINTEVRSFGVSRSGFTLAFQDYGCGMSLIVAVFY 180
Db 121 WVKVDTIADESFQVDLGGVMMKINTEVRSFGVSRSGFTLAFQDYGCGMSLIVAVFY 180
QY 181 RKCPRILONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 240
Db 181 RKCPRILONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 240
QY 241 MCKAGFEAVENGTCVRCGCPSPGTFKANGDDEACTHCPINSRTTSEGAATNCVCRNGYTRADL 300
Db 241 MCKAGFEAVENGTCVRCGCPSPGTFKANGDDEACTHCPINSRTTSEGAATNCVCRNGYTRADL 300
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Db 301 DPLMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSCSGRGACTR 360
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Db 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDSPSPQFASVNIITNOA 420
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Db 421 APSAVSIMHOVSTVDSITLSWSQDPQNGVILIDYELQYEEKELSEYNATAIKSPNTVT 480
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Db 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEYQTSIOEKPLIIGSSAAGLVFLI 540
QY 541 AVVVIAT 547
Db 541 AVVVIAT 547

RESULT 3
PCT-US95-04681-11
; Sequence 11, Application PC/TU9504681
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04681
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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MOLECULE TYPE: protein
PCP-US95-04681-11

Query Match 100.0% Score 2895; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 5.5e-246;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAARETLDSTTAAELGMVHPSPGMEVSGYDENMTIRTYOVAVFESSQNNMLR 60
DB 1 LLAARETLDSTTAAELGMVHPSPGMEVSGYDENMTIRTYOVAVFESSQNNMLR 60
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DB 61 TKTIRRGARHRIHVEKFSVRDCCSIPSPGSKETFNLYYEADFSATYTPMMENP 120
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DB 121 WVKVDTIADESEFQVLDGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 180
QY 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDEMLVPIGR 240
DB 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDEMLVPIGR 240
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DB 241 MCKAGEAVENGTVCRCGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
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DB 301 DPLDMPTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
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DB 361 CGDNVOYAPROLGLEPRITISDLAHTQYFEIOAVNGVTDQSPFSPQFASVITITNOA 420
QY 421 APSAVSIHVOVSRTVDSITLSMSOPDQNGVILDELYEKEKSEYNATIKSPNTVT 480
DB 421 APSAVSIHVOVSRTVDSITLSMSOPDQNGVILDELYEKEKSEYNATIKSPNTVT 480
QY 481 GLKAGAIYFQVARTVAGYGRSGKMYFQMTAEAYOTSIQEKPLIIGSSAAGLVFLI 540
DB 481 GLKAGAIYFQVARTVAGYGRSGKMYFQMTAEAYOTSIQEKPLIIGSSAAGLVFLI 540
QY 541 AVVVIAI 547
DB 541 AVVVIAI 547

US-08-542-635-2
Sequence 2, April 1998, US/08542635
Patent No. 6230856
GENERAL INFORMATION:
APPLICANT: Pawsan, Anthony
APPLICANT: Henkemeier, Mark
TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: 40 King Street West, Box 401
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2

CLM 2-548
26-548
4/29/94
CLM 5
PRIORITY
TO

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/542,635
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McDiarmid, Shona S.
REGISTRATION NUMBER: 38,798
REFERENCE/DOCKET NUMBER: 3153-162
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
TELEX: 06-23115
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:
LIBRARY: lambda gt10 cDNA library
CLONE: Combined pNKRACE A2 and K2 and cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Distal end of chromosome 4
MAP POSITION: near the and-1 mutation
US-08-542-635-2

Query Match 99.1% Score 2870; DB 4; Length 994;
Best Local Similarity 98.9%; Pred. No. 8.9e-244;
Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

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DB 23 LLAARETLDSTTAAELGMVHPSPGMEVSGYDENMTIRTYOVAVFESSQNNMLR 82
QY 61 TKTIRRGARHRIHVEKFSVRDCCSIPSPGSKETFNLYYEADFSATYTPMMENP 120
DB 83 TKTIRRGARHRIHVEKFSVRDCCSIPSPGSKETFNLYYEADFSATYTPMMENP 142
QY 121 WVKVDTIADESEFQVLDGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 180
DB 143 WVKVDTIADESEFQVLDGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 202
QY 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDEMLVPIGR 240
DB 203 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDEMLVPIGR 262
QY 241 MCKAGEAVENGTVCRCGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
DB 263 MCKAGEAVENGTVCRCGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 322
QY 301 DPLDMPTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
DB 323 DPLDMPTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 382
QY 361 CGDNVOYAPROLGLEPRITISDLAHTQYFEIOAVNGVTDQSPFSPQFASVITITNOA 420
DB 383 CGDNVOYAPROLGLEPRITISDLAHTQYFEIOAVNGVTDQSPFSPQFASVITITNOA 442
QY 421 APSAVSIHVOVSRTVDSITLSMSOPDQNGVILDELYEKEKSEYNATIKSPNTVT 480
DB 443 APSAVSIHVOVSRTVDSITLSMSOPDQNGVILDELYEKEKSEYNATIKSPNTVT 502
QY 481 --GLKAGAIYFQVARTVAGYGRSGKMYFQMTAEAYOTSIQEKPLIIGSSAAGLVFLI 538
DB 503 VGLKAGAIYFQVARTVAGYGRSGKMYFQMTAEAYOTSIQEKPLIIGSSAAGLVFLI 562
QY 539 LIAVVIAI 547
DB 563 LIAVVIAI 571

RESULT 5
 US-08-162-809-18
 Sequence 18, Application US/08162809
 Patent No. 5457048
 GENERAL INFORMATION:
 APPLICANT: Pasquale, Elena B.
 APPLICANT: Sajjadi, Fereydoon G.
 TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CAMPBELL AND FLORES
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States of America
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentia Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/162,809
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 9503
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-8901
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 995 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-162-809-18
 Query Match 96.2%; Score 2785; DB 1; Length 995;
 Best Local Similarity 94.5%; Pred. No. 2,7e-236;
 Matches 519; Conservative 19; Mismatches 9; Indels 2; Gaps 1;
 QY 1 LLAAEVETLMSTATAATAGLGMVHPSPGWEVERVSGYDENNTTIRTYOYCNVFESSONMRLR 60
 DB 23 LLAAEVETLMSTATAATAGLGMVHPSPGWEVERVSGYDENNTTIRTYOYCNVFESSONMRLR 82
 QY 61 TKFTIRRAAHRIHVMKRSYRDCSSIPSPVPSCKEFTENLYYYEADFPSATKTPPNMKNENP 120
 DB 83 TKYIRRAHRIHVMKRSYRDCSSIPSPVPSCKEFTENLYYYEADFPSATKTPPNMKNENP 142
 QY 121 WKYVDITIADESFQVDIGGRVMKINTEVRSFGVPSRSGFYLAQDYGGCMLIAVREY 180
 DB 143 WKYVDITIADESFQVDIGGRVMKINTEVRSFGVPSRSGFYLAQDYGGCMLIAVREY 202
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 DB 203 RKCPRIIONGAIFOTLSGAEASTSLVAARSGCINNAEVDVPIKLYONGGEMLPVIGRC 262
 QY 241 MKKAGEAENVTGVRGPGSGTFKANOQDEACTHCPIINSRTTSGATNCVCRNGYRADL 300
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 QY 301 DELIDMPCCTTIPSAPOAVISSVNETSILMLEWTPPRDSSGREDLVYNIICKSGSGRGACTR 360
 DB 323 DVAIDMPCCTTIPSAPOAVISSVNETSILMLEWTPPRDSSGREDLVYNIICKSGSGRGACTR 382
 QY 361 GGDNVQIAPARQUGLIEPRIRYISDLAHQYIFELQAVNGVTDQSPFSQGFASVNIITNQ 420

Dec. 3, 1993

Db	383	CGDNVQFAPRQGLITEPRIYISDLIAHTQVTFELQAVNGVTDGSPSPQASVNIITNOA	442
QY	421	APSAVSIIMHGVSRIVSITSLWSOPDPNGVILIDELQYKEKLESEYNATAIKSPINVTY	480
Db	443	APSAVSIIMHGVSRIVSITSLWSOPDPNGVILIDELQYKEKNISELINSAVSPINVTY	502
QY	481	--GLKAAITVFQVARTVAGVGRYSKMTFQMTAEAYQTSIOEKPLITIGSSAGLVF	538
Db	503	VQNKIAITVFQVARTVAGVGRYSKMTFQMTAEAYQTSIOEKPLITIGSSAGLVF	562
QY	539	LIAVVIAT 547	
Db	563	LIAVVIAT 571	
RESULT	6		
	US-08-162-809-12		
	Sequence 12, Application US/08162809		
	Patent No. 5457048		
	GENERAL INFORMATION:		
	APPLICANT: Pasquale, Elena B.		
	APPLICANT: Sajjadi, Fereydoun G.		
	TITLE OF INVENTION: NOVEL Eph-RELATED TYROSINE KINASES.		
	TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE		
	NUMBER OF SEQUENCES: 26		
	CORRESPONDENCE ADDRESSES:		
	ADDRESS: CAMPBELL AND FLORES		
	STREET: 4370 La Jolla Village Drive, Suite 700		
	CITY: San Diego		
	STATE: California		
	COUNTRY: United States of America		
	ZIP: 92122		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: Floppy disk		
	COMPUTER: IBM PC compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS		
	SOFTWARE: PatentIn Release #1.0, Version #1.25		
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER: US/08/162,809		
	FILING DATE:		
	CLASSIFICATION: 514		
	ATTORNEY/AGENT INFORMATION:		
	NAME: Campbell, Cathryn A.		
	REGISTRATION NUMBER: 31,815		
	REFERENCE/DOCKET NUMBER: P-LJ 9503		
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE: (619) 535-9001		
	TELEFAX: (619) 535-8949		
	INFORMATION FOR SEQ ID NO: 12:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH: 1011 amino acids		
	TYPE: amino acid		
	TOPOLOGY: linear		
	MOLECULE TYPE: protein		
	US-08-162-809-12		
Query Match	96.2%	Score 2785;	DB 1; Length 1011;
Best Local Similarity	94.5%;	Pred. No. 2.7e-236;	
Matches 519; Conservative	19;	Mismatches 9;	Indels 2; Gaps 1;
QY	1	LAAAEETIMDSSTTATAEAGMWHPSPGMEVSGYDENNTIRTYQCVNVESSONNMR	60
Db	23	LAAAEETIMDSSTTATAEAGMWHPSPGMEVSGYDENNTIRTYQCVNVESSONNMR	82
QY	61	TYFIRRRGAHRITHEKKEFSYRDCSSITPSVPGSCKEFNLXYEADPDSATKTFPMNMEP	120
Db	83	TKYIRRRGAHRITHEKKEFSYRDCSSITPNVPGSCKEFNLXYEADPDSATKTFPMNMEP	142
QY	121	WVAVDITLADSESFQVILGGRVAKITTEVRSFGPVSRSGFYLAFODYGGCMLIAVRVFY	180
Db	143	WVAVDITLADSESFQVILGGRVAKITTEVRSFGPVSRSGFYLAFODYGGCMLIAVRVFY	202

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OY 181 RCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGMVPIGRG 240
DB 203 RCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGMVPIGRG 262
OY 241 MCKAGFEAVENGTCVRCGCPGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
DB 263 MCRPGYEVSENGTCVRCGCPGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 322
OY 301 DPLDMPCTTIPSAPOAVISVNETSLMEWTTPRDSGGREDLVYNIICKSCSGSGGACTR 360
DB 323 DPLDMPCTTIPSAPOAVISVNETSLMEWTTPRDSGGREDLVYNIICKSCSGSGGACTR 382
OY 361 CGDNVOYAPROLGTEPRITISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 420
DB 383 CGDNVOYAPROLGTEPRITISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 442
OY 421 APSAIVSIMHOVSRTVDSITLSMSQDPDQNGVILDELOYEKEKELSEYNATAIKSPNTVT 480
DB 443 APSAIVSIMHOVSRTVDSITLSMSQDPDQNGVILDELOYEKEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFQVARTVAGYGRYSKMYFOTMTEAEYOTSIOEKLPLIIGSSAAGLVF 538
DB 503 VONLAKAGTIYFQVARTVAGYGRYSKMYFOTMTEAEYOTSIOEKLPLIIGSSAAGLVF 562
OY 539 LIAVVVIAI 547
DB 563 LIAVVVIAI 571

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524, 1994

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RESULT 7
US-08-673-789-5
; Sequence 5, Application US/08673789
; Patent No. 5814479
; GENERAL INFORMATION:
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
; APPLICANT: GEORGE, F.
; TITLE OF INVENTION: BSK RECEPTOR LIKE
; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,789
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/177,812
; FILING DATE: 04-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPP
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO. 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 995

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; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; US-08-673-789-5

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Query Match 95.3%; Score 2758; DB 2; Length 995;
Best Local Similarity 93.6%; Pred. No. 6,3e-234;
Matches 514; Conservative 19; Mismatches 14; Indels 2; Gaps 1;

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OY 1 LIAVEETLNDSTTATPELGMVHPSPGMEVSGYDENMTITTYQVCNVESSONNMLR 60
DB 23 LIAVEETLNDSTTATPELGMVHPSPGMEVSGYDENMTITTYQVCNVESSONNMLR 82
OY 61 TKFIRRRGARIRHVEKMFVSRDCSSIPSVGSCKETFNLYYEADPDASATKTPNNMNP 120
DB 83 TKYIRRRGARIRHVEKMFVSRDCSSIPSVGSCKETFNLYYEADPDASATKTPNNMNP 142
OY 121 WNVVDITADESFQVDLGRVVKINTEVRSFGPVRSRGFYLAFOYGCMSLIAVVEY 180
DB 143 WNVVDITADESFQVDLGRVVKINTEVRSFGPVRSRGFYLAFOYGCMSLIAVVEY 202
OY 181 RCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGMVPIGRG 240
DB 203 RCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGMVPIGRG 262
OY 241 MCKAGFEAVENGTCVRCGCPGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
DB 263 MCRPGYEVSENGTCVRCGCPGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 322
OY 301 DPLDMPCTTIPSAPOAVISVNETSLMEWTTPRDSGGREDLVYNIICKSCSGSGGACTR 360
DB 323 DPLDMPCTTIPSAPOAVISVNETSLMEWTTPRDSGGREDLVYNIICKSCSGSGGACTR 382
OY 361 CGDNVOYAPROLGTEPRITISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 420
DB 383 CGDNVOYAPROLGTEPRITISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 442
OY 421 APSAIVSIMHOVSRTVDSITLSMSQDPDQNGVILDELOYEKEKELSEYNATAIKSPNTVT 480
DB 443 APSAIVSIMHOVSRTVDSITLSMSQDPDQNGVILDELOYEKEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFQVARTVAGYGRYSKMYFOTMTEAEYOTSIOEKLPLIIGSSAAGLVF 538
DB 503 VONLAKAGTIYFQVARTVAGYGRYSKMYFOTMTEAEYOTSIOEKLPLIIGSSAAGLVF 562
OY 539 LIAVVVIAI 547
DB 563 LIAVVVIAI 571

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RESULT 8
US-08-673-789-6
; Sequence 6, Application US/08673789
; Patent No. 5814479
; GENERAL INFORMATION:
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
; APPLICANT: GEORGE, F.
; TITLE OF INVENTION: BSK RECEPTOR LIKE
; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK

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16 TAEIGMWHPPSGWEEVSGYDENMTITPTTYQVCNFFESSQNNMLRTKFIIRRGAAHRIHVE 75

21 TSELAWTHETGWEVSGYDEAMNPIRTYQVCNAREANQNNMRTKEIQRDQVRVVE 80

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QY 76 MKEFVROGSSIPVVGSGKETFNLYYYEADPDASATKTFPMNMENPVKVDITIADESFQ 135
DB 81 LKFTYRDCNSIPNIPGSKETFNLFYTSDDSDSANSFPMENPVKVDITIADESFQ 140
QY 136 VDLGRVVKINTEVRSFGVRSRGFYLAFOYGGCMSTIAVRVYRKCPRILOKALFOE 195
DB 141 LESG----RVNTKVRSFGPLSKNGFYLAFODLGACMSLISVRAFKCSNLTAGFALPPE 196
QY 196 TUSGAEHSISVAARSCIANEVEVDPPIKICONGGEMLVPIGRCMKAFGEAVENGTVG 255
DB 197 TLTGAEPSISLVAPTCTCPNAVEVPLKICONGGEMVVPVGACTCAAGEPAMKDTQC 256
QY 256 RCPGSGTEKANOGBACTHCPINSTRITSEGATNCYCRNGYRADIDPLDMPCTTIPSAPO 315
DB 257 QACGCTGFSKQGEBCSPCPNSRTAGATVYCISGSEFRADADPADSACTVPSAPR 316
QY 316 AVTSYNETSLMEWTPPDSDGREDLVYNIICKSGSGRACCTGCGDVQVAPROL--- 372
DB 317 SVISYNETSLVLEWSEPODAGRDLDLYNICKKCSYERLCSRDNDVETVPRLGLIT 376
QY 373 GLTEPRITISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOAPSASVSTMHVS 432
DB 377 GLTERITISYKWAHPQYTFEIOAVNGISSKSPYRPHFASVNTTNOAPSASVPTMHLHS 436
QY 433 RIVDSITLSKSDPQNGVILDELOYEKE--LSEYNATAISPTNTV--TGLKGAIVY 489
DB 437 STGNSMTLSMTPEPENGIIIDYEIKYSKOGDGIANTVTSQKNSLDLGLKANAKRM 496
QY 490 FOVRATVAGYGYRSGKMYFQUTMEAYOTSIQIEKPLIIGSSAAGVELLAVVIAI 547
DB 497 VOVRATVAGYGRSLPTEPQTAEQGSISKTPQELPLIVGSAATALLVIVVIAI 554

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RESULT 12
US-08-449-645A-20
; Sequence 20, Application US/08449645A
; Patent No. 5981245
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-449-645A-20

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Query Match 62.2%; Score 1800.5; DB 2; Length 998;
Best Local Similarity 61.9%; Pred. No. 1e-149;

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Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;
QY 4 AVETLMDSTTAAELGRMYHPPSGHEEYSGYDENMTIRTOVCNVFPSSNNMLRTKF 63
DB 37 ALBETLMDTKWTSSELATVSHPSGHEEYSGYDEAMPKTIYOVNVRESSNNMLRTGF 96
QY 64 IRRGARIRHVEKFSVDCSIPVVGSGKETFNLYYYEADPDASATKTFPMNMENPVK 123
DB 97 IWRDVORVYVELKFTYRDCNSIPNIPGSKETFNLFYTSDDSDSANSFPMENPVK 156
QY 124 VDTIADESESQVDLGRVVKINTEVRSFGVRSRGFYLAFOYGGCMSTIAVRVYRK 183
DB 157 VDTIAPDESEFRLDAG---RVNTKVRSFGPLSKNGFYLAFOGACMSLISVRAFKKC 212
QY 184 PRIIONAIFQETLSGAPSTISVAARSCIANEVEVDPPIKICONGGEMLVPIGRCMK 243
DB 213 ASTAGFALPPEITLGAHPISLVAPTCTCPNAVEVPLKICONGGEMVVPVGACTCA 272
QY 244 AGFEAVENGTVGRCGCPGSGTEKANOGBACTHCPINSTRITSEGATNCYCRNGYRADIDPL 303
DB 273 TGHEPAKESQCRCPSPSYKAKQGEBCPLCPCPNSRTISPAASICTCHNNFTRAUSD 332
QY 304 DMPCTTIPSAPOYISSYNETSLMEWTPPDSDGREDLVYNIICKSC--GSGRGACTRC 361
DB 333 DSACTVPSPPRGVYSYNETSLMEWSEPRDLGVRDLDLYNICKKCHGAGSACSRC 392
QY 362 GDNVOYARQLGLEPRITISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 421
DB 393 DNVETVYRQLGSLSPRHTSHLAAHTYTFEIOAVNGVSGKSPLPYRAVNTTNOA 452
QY 422 PSAVIMHVSRTVDSITLSMSQDPQNGVILDELOYEKE--LSEYNATAISPTNTV-- 479
DB 453 PSEVPTLRHSSGSSLSLWNAPEPENGVIDYEKKEF--SEGASITVTSQKNSLD 510
QY 480 TGLKGAIVYFQVRATVAGYGRSGKMYFQUTMEAYOTSIQIEKPLIIGSSAAGIV 538
DB 511 DGLRDPARTVVOVRATVAGIGYSPALFETTSBRSQAQDLQELPLIVGSAATAGIV 570
QY 539 LIAVVVIAI 547
DB 571 VAVVIVIAI 579

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RESULT 13
US-08-702-367A-20
; Sequence 20, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:

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LENGTH: 998 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-702-367A-20

Query Match 62.2%; Score 1800.5; DB 2; Length 998;
 Best Local Similarity 61.9%; Pred. No. 1e-149;
 Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTTATAEIGMWHPPSGMEVSGYDENNTIRTYOVCNPFESSQNNMLRTKF 63
 DB 37 ALEETLMDTKWTSLELAWTSHPESGMEVSGYDEAMNPIRTYQVCNPFESSQNNMLRTGF 96
 QY 64 IRRGCAHRIHVEKESFVSDCSIPSVGSKETFNLYYEADFDSTAKTFPMNMENPMVK 123
 DB 97 IWRDQVQRYVELKFTYVDCNSIPNIPGSKETFNLYYEADSDVASASSPFMMENPMYK 156
 QY 124 VDTIADESFQVDLGGVWKINTEVSRGPFVSRGFYLAPODYGCGMSLAVRFFRK 183
 DB 157 VDTIAPDESFRDLAG---RVNTKVRSGFPLSKAGFYLAPODQACMSLISVRAFFRK 212
 QY 184 PRIIONGAIFOETLSGAEISTLVAAAGSCIANAEEDVPILKYCNGDEMLVPIGRCK 243
 DB 213 ASTAGFALFPELTIGAEPTSLVIAPGTCIPNAVEVSPLKLYCNGDEMLVPIGACTCA 272
 QY 244 AGFEAVENGTVRCGPGSTGRKANGDEACTHCPINSTTSEGATNCYCRNGYRADLPL 303
 DB 273 TGHPRAKESGCRCPGSKAKGEGPCLPCPPNSRTTSPASISICCHNNFYRADSDSA 332
 QY 304 DMCPTTIPSAPOAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSC--GSGRGACTR 361
 DB 333 DSACTTVPSPRGVYSVNETSLILEMSEPRDLGVRDLLYNICKKHGAGASACSRK 392
 QY 362 GDNVQYARQLGLTPRIYISDLAHQYTFEIQAVNGVTDOSSPQFASVNTTNOAA 421
 DB 393 DDNVEFVRQLGLSEPRVHTSHLAHTRYFEVQAVNGVSGKSLPRRYAAVNTTNOAA 452
 QY 422 PSAVSIMHOVSRVDSITLSMSOPDPNGVILDELOYKEKELSEYNATKSPNTV-- 479
 DB 453 PSEVPTLRLHSSGSSSLTSLNAPPERNGVILDEYEMKFEK--SEGIASTYTSQNNVOL 510
 QY 480 TGLKAGAIYFQVRAVAGYGRSGKMFQJMTF-AEYQTSIOEKPLITIGSSAAGLV 538
 DB 511 DGLRPARYVQVRAVAGYGRSGKMFQJMTF-AEYQTSIOEKPLITIGSSAAGLV 570
 QY 539 LIAVVYVIAI 547
 DB 571 VVAVVYVIAI 579

RESULT 14
 PCT-US95-04681-20
 Sequence 20, Application PC/TUS9504681
 GENERAL INFORMATION:

APPLICANT: Fox, Gary M.
 TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Patent Operations/RBH
 STREET: 1840 Dehavenland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04681
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Robert B.
 REFERENCE/DOCKET NUMBER: A-287
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 998 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-04681-20

Query Match 62.2%; Score 1800.5; DB 5; Length 998;
 Best Local Similarity 61.9%; Pred. No. 1e-149;
 Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTTATAEIGMWHPPSGMEVSGYDENNTIRTYOVCNPFESSQNNMLRTKF 63
 DB 37 ALEETLMDTKWTSLELAWTSHPESGMEVSGYDEAMNPIRTYQVCNPFESSQNNMLRTGF 96
 QY 64 IRRGCAHRIHVEKESFVSDCSIPSVGSKETFNLYYEADFDSTAKTFPMNMENPMVK 123
 DB 97 IWRDQVQRYVELKFTYVDCNSIPNIPGSKETFNLYYEADSDVASASSPFMMENPMYK 156
 QY 124 VDTIADESFQVDLGGVWKINTEVSRGPFVSRGFYLAPODYGCGMSLAVRFFRK 183
 DB 157 VDTIAPDESFRDLAG---RVNTKVRSGFPLSKAGFYLAPODQACMSLISVRAFFRK 212
 QY 184 PRIIONGAIFOETLSGAEISTLVAAAGSCIANAEEDVPILKYCNGDEMLVPIGRCK 243
 DB 213 ASTAGFALFPELTIGAEPTSLVIAPGTCIPNAVEVSPLKLYCNGDEMLVPIGACTCA 272
 QY 244 AGFEAVENGTVRCGPGSTGRKANGDEACTHCPINSTTSEGATNCYCRNGYRADLPL 303
 DB 273 TGHPRAKESGCRCPGSKAKGEGPCLPCPPNSRTTSPASISICCHNNFYRADSDSA 332
 QY 304 DMCPTTIPSAPOAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSC--GSGRGACTR 361
 DB 333 DSACTTVPSPRGVYSVNETSLILEMSEPRDLGVRDLLYNICKKHGAGASACSRK 392
 QY 362 GDNVQYARQLGLTPRIYISDLAHQYTFEIQAVNGVTDOSSPQFASVNTTNOAA 421
 DB 393 DDNVEFVRQLGLSEPRVHTSHLAHTRYFEVQAVNGVSGKSLPRRYAAVNTTNOAA 452
 QY 422 PSAVSIMHOVSRVDSITLSMSOPDPNGVILDELOYKEKELSEYNATKSPNTV-- 479
 DB 453 PSEVPTLRLHSSGSSSLTSLNAPPERNGVILDEYEMKFEK--SEGIASTYTSQNNVOL 510
 QY 480 TGLKAGAIYFQVRAVAGYGRSGKMFQJMTF-AEYQTSIOEKPLITIGSSAAGLV 538
 DB 511 DGLRPARYVQVRAVAGYGRSGKMFQJMTF-AEYQTSIOEKPLITIGSSAAGLV 570
 QY 539 LIAVVYVIAI 547
 DB 571 VVAVVYVIAI 579

RESULT 15
 US-08-348-143-1
 Sequence 1, Application US/08348143
 Patent No. 5506205
 GENERAL INFORMATION:

APPLICANT: TAJIMA, HISAO
 APPLICANT: KITAGAWA, KOICHIRO
 APPLICANT: OHNO, HIROYUKI
 APPLICANT: UENO, TOSHIO
 TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein p140 and DNAs
 encoding it

NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037-3202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/348,143
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 315806/1993
 FILING DATE: 24-NOV-1993
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)293-7060
 TELEFAX: (202)293-7860
 TELEX: 6491103
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 993 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORGANISM: rat
 TISSUE TYPE: skeletal muscle myoblast
 CELL LINE: L6
 US-08-348-143-1

Query Match 61.0%; Score 1765.5; DB 1; Length 993;

Best Local Similarity 58.9%; Pred. No. 1.2e-146; Matches 336; Conservative 80; Mismatches 123; Indels 31; Gaps 6;

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 166 DYGCMSLIVRVFRYKCPRIIONGALFQETLSGAESTSLVAARGSCIANAEVDPYIKL 225
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 427 SKSPLPRYIAVNTITNOAAPSEVPTLHLHSSGSSITLSMAPPERPNGVILDYEMKYF 486

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 DB 545 AAOIQEOLPIIVGSTVAGFVFMVVVVIAL 574

Search completed: February 1, 2002, 09:56:30
 Job time: 210 sec

Fri Feb 1 11:16:37 2002

us-09-378-759-11_copy_1_547.rai

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 1, 2002, 09:59:42 : Search time 192.18 Seconds

(without alignments)
790.292 Million cell updates/sec

Title: US-09-378-759-11_COPY_1_547

Sequence: 2895
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Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 3148936 segs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2895	100.0	970	8	US-08-449-645-11
2	2895	100.0	970	11	US-08-702-367-11
3	2895	100.0	970	17	US-09-378-759-11
4	2870	99.1	994	6	US-08-235-407-2
5	2870	99.1	994	11	US-08-727-463-2
6	2870	99.1	994	11	US-08-727-463-2
7	2870	99.1	994	11	US-08-730-700-2
8	2870	99.1	994	11	US-08-730-700A-2
9	2870	99.1	994	20	US-09-621-595-2

10	2078.5	71.8	990	15	US-09-194-755A-7	Sequence 7, App1
11	1976	68.3	1009	3	US-07-861-390D-6	Sequence 6, App1
12	1800.5	62.2	998	8	US-08-449-645-20	Sequence 20, App1
13	1800.5	62.2	998	11	US-08-702-367-20	Sequence 20, App1
14	1800.5	62.2	998	17	US-09-378-759-20	Sequence 20, App1
15	1799.5	62.2	1007	1	PCT-US01-03800A-2273	Sequence 2273, App
16	1799.5	62.2	999	24	US-60-201-702-1172	Sequence 172, App
17	1789.5	61.8	961	24	US-60-200-366-202	Sequence 202, App
18	1789.5	61.8	961	24	US-60-201-702-165	Sequence 165, App
19	1765.5	61.0	993	19	US-09-558-340-1	Sequence 1, App1
20	1753	60.6	559	24	US-60-206-106-122	Sequence 122, App
21	1743.5	60.2	951	24	US-60-205-421-278	Sequence 278, App
22	1728.5	59.7	954	24	US-60-205-421-275	Sequence 275, App
23	1689.5	58.4	911	24	US-60-201-702-173	Sequence 21, App1
24	1687.5	58.3	1002	15	US-09-194-755A-6	Sequence 6, App1
25	1671	57.7	908	24	US-60-200-366-211	Sequence 211, App
26	1671	57.7	908	24	US-60-201-702-161	Sequence 161, App
27	1614	55.8	947	24	US-60-201-702-166	Sequence 166, App
28	1582	54.6	905	24	US-60-205-421-289	Sequence 289, App
29	1580	54.6	889	24	US-60-201-702-162	Sequence 162, App
30	1485.5	51.3	993	21	US-09-751-389-7	Sequence 7, App1
31	1485.5	51.3	967	17	US-09-378-759-13	Sequence 13, App1
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35	1485.5	51.3	991	17	US-09-378-759-13	Sequence 13, App1
36	1485.5	51.3	991	22	US-09-823-187-44	Sequence 187, App
37	1482.5	51.2	666	21	US-09-771-161-136	Sequence 136, App
38	1482.5	51.2	983	1	PCT-US00-04326-3	Sequence 3, App1
39	1482.5	51.2	983	21	US-09-771-161A-136	Sequence 227, App
40	1482.5	51.2	983	21	PCT-US00-04326-5	Sequence 103, App
41	1482.5	51.2	983	21	US-09-771-161A-136	Sequence 6, App1
42	1481	51.2	1005	5	US-08-144-992-103	Sequence 21, App1
43	1478.5	51.1	968	8	US-09-751-389-6	Sequence 8, App1
44	1476.5	51.0	983	21	US-08-449-645-21	Sequence 21, App1
45	1476.5	51.0	983	11	US-08-702-367-21	Sequence 21, App1

ALIGNMENTS

RESULT 1
US-08-449-645-11
Sequence 11, Application US/08449645
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
APPLICANT: Welcher, Andrew A.
APPLICANT: Jiny, Shuguan
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Amgen Patent Operations/RBW
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645
FILING DATE: May 24, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287-A
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645-11

Query Match 100.0%; Score 2895; DB 8; Length 970;
Best Local Similarity 100.0%; Pred. No. 2,5e-261;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 WKVDTIADESFQVDLGGRYMKINTEVRSFGVSRSGFYLAFOYGGCMLAVRVFY 180
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DB 181 RKCPTIIONGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDEMLVPIGRC 240
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DB 481 GLKAGAIYVQVARTVAGYGRYSGRMYPQMTAEAYQTSIOEKPLIIGSSAAGLVFLI 540
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DB 541 AVVVIAI 547
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RESULT 2
US-08-702-367-11
Sequence 11, Application US/08702367
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367

FILING DATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,509
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367-11

Query Match 100.0%; Score 2895; DB 11; Length 970;
Best Local Similarity 100.0%; Pred. No. 2,5e-261;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 TFFIRRGARHRIHEMKFSVRDCSSIPSPGCKEFTNLYYEADPDSATKTPNNMNEP 120
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DB 421 APSAVSIMHOVSRTVDSITLSWSOPDPQNGVILIDYELQYKEKLESEYNATAIKSPNTVT 480
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DB 481 GLKAGAIYVQVARTVAGYGRYSGRMYPQMTAEAYQTSIOEKPLIIGSSAAGLVFLI 540
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DB 541 AVVVIAI 547
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RESULT 3
US-09-378-759-11
Sequence 11, Application US/09378759
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBM
STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/378,759
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-378-759-11

Query Match 100.0%; Score 2895; DB 17; Length 970;
Best Local Similarity 100.0%; Pred. No. 2.5e-261;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-08-235-407-2

Sequence 2, Application US/08235407
GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
APPLICANT: Henkemeyer, Mark
TITLE OF INVENTION: NOVEL NEURAL KINASE AND RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West, Box 401
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,407
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kurydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-82
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
FILER: 06-23115
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:
LIBRARY: lambda gt10 cDNA library
CLONE: Combined pNKRACE A2 and K2 and cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Distal end of chromosome 4
MAP POSITION: near the ahd-1 mutation
US-08-235-407-2

Query Match 99.1%; Score 2870; DB 6; Length 994;
Best Local Similarity 98.9%; Pred. No. 5.7e-259;
Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

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83 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYEADPDSAKTTPNNMEMP 142
121 WVKVDITAADESFQVDLGRVVKINTEVRSPGVRSGFYLAFOYGGCMLIAVRVY 180
121 WVKVDITAADESFQVDLGRVVKINTEVRSPGVRSGFYLAFOYGGCMLIAVRVY 180
143 WVKVDITAADESFQVDLGRVVKINTEVRSPGVRSGFYLAFOYGGCMLIAVRVY 202
181 RKCPRITONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRG 240
203 RKCPRITONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRG 262

```

OY 241 MCKAGFEAVENGTCRCGPGCTFRKANGDEACTHCPINSRTSGATNCYCRNGYRADL 300
Db 263 MCKAGFEAVENGTCRCGPGCTFRKANGDEACTHCPINSRTSGATNCYCRNGYRADL 322
OY 301 DPLMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
Db 323 DPLMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 382
OY 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTTNOA 420
Db 383 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTTNOA 442
OY 421 APSAVSIMHOVSRTVDSITLSMSQPDQPNVILDYELQYKEKELSEYNATAIKSPNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLSMSQPDQPNVILDYELQYKEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFQVBARVYAGRGYSKMYQTMTAEAYOTSIQKELPLIGSSAAGLVF 538
Db 503 VQGLKAGAIYFQVBARVYAGRGYSKMYQTMTAEAYOTSIQKELPLIGSSAAGLVF 562
OY 539 LIAVVVIAI 547
Db 563 LIAVVVIAI 571

```

RESULT 5

```

US-08-727-463-2
; Sequence 2, Application us/08727463
; GENERAL INFORMATION:

```

```

APPLICANT: PAMSON, Anthony
APPLICANT: Henkemeyer, Mark
APPLICANT: Letwin, Kenneth
TITLE OF INVENTION: NEURAL RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: MERCHANT & GOULD
STREET: 3100 Northwest Center, 90 South Seventh Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: U.S.A.
ZIP: 55403-4131

```

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,463
FILING DATE: 18-OCT-1996
CLASSIFICATION: 800

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: M&G 7933.89-US-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 332-5300
TELEFAX: (612) 332-9081

```

INFORMATION FOR SEQ ID NO: 2:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:
LIBRARY: lambda gt10 cDNA library
CLONE: Combined pNURACE A2 and K2 and cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Distal end of chromosome 4
MAP POSITION: near the ahd-1 mutation

```

US-08-727-463-2

```

Query Match          99.1%; Score 2870; DB 11; Length 994;
Best local Similarity 98.9%; Pred. No. 5,7e-259;
Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

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OY 1 LIAVETLMDSTTATTAELGMMVHPSPGMEVEVSGYDENNTIRTYOVAVFESSQNNMLR 60
Db 23 LIAVETLMDSTTATTAELGMMVHPSPGMEVEVSGYDENNTIRTYOVAVFESSQNNMLR 82
OY 61 TKFIRRGARHIREVEMKFSYRDCSSIPYVPGCKETFFNLITYEADPDSATKTFPMNMEHP 120
Db 83 TKFIRRGARHIREVEMKFSYRDCSSIPYVPGCKETFFNLITYEADPDLATKTFPMNMEHP 142
OY 121 WVKYDTIAADESFQVDLGGRVKMTNTEVRSFGPVRSGFYLAFOYGGCMSLIAVRVY 180
Db 143 WVKYDTIAADESFQVDLGGRVKMTNTEVRSFGPVRSGFYLAFOYGGCMSLIAVRVY 202
OY 181 RKPRIITONGAIFQETLSGAESTSLVAARSGCIANAEVDVPIKLYCNGDEMLVPIGRG 240
Db 203 RKPRIITONGAIFQETLSGAESTSLVAARSGCIANAEVDVPIKLYCNGDEMLVPIGRG 262
OY 241 MCKAGFEAVENGTCRCGPGCTFRKANGDEACTHCPINSRTSGATNCYCRNGYRADL 300
Db 263 MCKAGFEAVENGTCRCGPGCTFRKANGDEACTHCPINSRTSGATNCYCRNGYRADL 322
OY 301 DPLMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
Db 323 DPLMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 382
OY 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTTNOA 420
Db 383 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTTNOA 442
OY 421 APSAVSIMHOVSRTVDSITLSMSQPDQPNVILDYELQYKEKELSEYNATAIKSPNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLSMSQPDQPNVILDYELQYKEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFQVBARVYAGRGYSKMYQTMTAEAYOTSIQKELPLIGSSAAGLVF 538
Db 503 VQGLKAGAIYFQVBARVYAGRGYSKMYQTMTAEAYOTSIQKELPLIGSSAAGLVF 562
OY 539 LIAVVVIAI 547
Db 563 LIAVVVIAI 571

```

RESULT 6

```

US-08-727-463-2
; Sequence 2, Application us/08727463A
; GENERAL INFORMATION:

```

```

APPLICANT: PAMSON, ANTHONY
APPLICANT: HENKEMEYER, MARK
APPLICANT: LETWIN, KENNETH
APPLICANT: MOUNT SINAI HOSPITAL CORPORATION
TITLE OF INVENTION: METHODS FOR IDENTIFYING SUBSTANCES AFFECTING RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE ACTIVITY (AS AMENDED)
FILE REFERENCE: 7933.89USWO
CURRENT APPLICATION NUMBER: US/08/727,463A
CURRENT FILING DATE: 1997-03-11
EARLIER APPLICATION NUMBER: PCT/CA95/00254
EARLIER FILING DATE: 1995-04-28
EARLIER APPLICATION NUMBER: 08/235,407
EARLIER FILING DATE: 1994-04-29

```

```

NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 994
TYPE: PRT
ORGANISM: Mus musculus

```

```

US-08-727-463-2

```


Query Match 99.1%; Score 2870; DB 11; Length 994;
 Best Local Similarity 98.9%; Pred. No. 5.7e-259;
 Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

```

OY 1 LLAAVETLMDSTTATATLGMVHPPSGMEVSGYDENNTIRTYOVNVESSONMLR 60
DB 23 LLAAVETLMDSTTATATLGMVHPPSGMEVSGYDENNTIRTYOVNVESSONMLR 82
OY 61 TKFIRRGARHRIHVEKFSVRDCCSIPVSGCKETFNLYYEADFDLTKTFPMNENP 120
DB 83 TKFIRRGARHRIHVEKFSVRDCCSIPVSGCKETFNLYYEADFDLTKTFPMNENP 142
OY 121 WVKVDTIADESFQVDLGRVAKINTEVRSRSGFYLAFODYGCMSLAVRVFY 180
DB 143 WVKVDTIADESFQVDLGRVAKINTEVRSRSGFYLAFODYGCMSLAVRVFY 202
OY 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPILKYCNGDEMLVPIGR 240
DB 203 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPILKYCNGDEMLVPIGR 262
OY 241 MCKAGEAVENGTCRGCPSTGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
DB 263 MCKAGEAVENGTCRGCPSTGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 322
OY 301 DPLDMCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
DB 323 DPLDMCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 382
OY 361 CGDNVOYAPROLGLEPRTIYISDLAHTOYFETIOAVNGVTDOSPFSPQASVNTTNOA 420
DB 383 CGDNVOYAPROLGLEPRTIYISDLAHTOYFETIOAVNGVTDOSPFSPQASVNTTNOA 442
OY 421 APSAVSINHQSRTVDSITLSMSOPDQNGVILDELOYEKELSEYNATAIKSPNTVT 480
DB 443 APSAVSINHQSRTVDSITLSMSOPDQNGVILDELOYEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFOVRAVAGYGRYSGKMYFOTTEAEYQTSIOEKPLITIGSSAGLVF 538
DB 503 VQGLKAGAIYFOVRAVAGYGRYSGKMYFOTTEAEYQTSIOEKPLITIGSSAGLVF 562
OY 539 LIAVVYIAI 547
DB 563 LIAVVYIAI 571

```

RESULT 7

US-08-730-700-2
 ; Sequence 2, Application US/08730700
 ; GENERAL INFORMATION:

APPLICANT: Pawson, Anthony
 TITLE OF INVENTION: Method of Activating a Novel Ligand
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bereskin & Parr
 STREET: 40 King Street West, Box 401
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/730,700
 FILING DATE:

CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydk, Linda M.

```

; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; TELEX: 06-23115
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Embryo
; IMMEDIATE SOURCE:
; LIBRARY: lambda gt10 cDNA library
; CLONE: Combined pNURACE A2 and K2 and cDNA clones
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Distal end of chromosome 4
; MAP POSITION: near the and-1 mutation
; US-08-730-700-2

```

Query Match 99.1%; Score 2870; DB 11; Length 994;
 Best Local Similarity 98.9%; Pred. No. 5.7e-259;
 Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

```

OY 1 LLAAVETLMDSTTATATLGMVHPPSGMEVSGYDENNTIRTYOVNVESSONMLR 60
DB 23 LLAAVETLMDSTTATATLGMVHPPSGMEVSGYDENNTIRTYOVNVESSONMLR 82
OY 61 TKFIRRGARHRIHVEKFSVRDCCSIPVSGCKETFNLYYEADFDLTKTFPMNENP 120
DB 83 TKFIRRGARHRIHVEKFSVRDCCSIPVSGCKETFNLYYEADFDLTKTFPMNENP 142
OY 121 WVKVDTIADESFQVDLGRVAKINTEVRSRSGFYLAFODYGCMSLAVRVFY 180
DB 143 WVKVDTIADESFQVDLGRVAKINTEVRSRSGFYLAFODYGCMSLAVRVFY 202
OY 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPILKYCNGDEMLVPIGR 240
DB 203 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPILKYCNGDEMLVPIGR 262
OY 241 MCKAGEAVENGTCRGCPSTGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
DB 263 MCKAGEAVENGTCRGCPSTGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 322
OY 301 DPLDMCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
DB 323 DPLDMCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 382
OY 361 CGDNVOYAPROLGLEPRTIYISDLAHTOYFETIOAVNGVTDOSPFSPQASVNTTNOA 420
DB 383 CGDNVOYAPROLGLEPRTIYISDLAHTOYFETIOAVNGVTDOSPFSPQASVNTTNOA 442
OY 421 APSAVSINHQSRTVDSITLSMSOPDQNGVILDELOYEKELSEYNATAIKSPNTVT 480
DB 443 APSAVSINHQSRTVDSITLSMSOPDQNGVILDELOYEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFOVRAVAGYGRYSGKMYFOTTEAEYQTSIOEKPLITIGSSAGLVF 538
DB 503 VQGLKAGAIYFOVRAVAGYGRYSGKMYFOTTEAEYQTSIOEKPLITIGSSAGLVF 562
OY 539 LIAVVYIAI 547
DB 563 LIAVVYIAI 571

```

RESULT 8

US-08-730-700A-2
 ; Sequence 2, Application US/08730700A

GENERAL INFORMATION:
 APPLICANT: Pawson, Anthony
 TITLE OF INVENTION: Method of Activating a Novel Ligand
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Room 970
 STREET: 600 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1X5

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/730,700A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/005,518
 FILING DATE: 13-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydyk, Linda M.
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-196
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 416-586-3235
 TELEFAX: 416-586-3110
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 994 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-730-700A-2

Query Match 99.1%; Score 2870; DB 11; Length 994;
 Best Local Similarity 98.9%; Pred. No. 5.7e-259;
 Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

1 LLAVEETLMDSTTATATLGMVHPPSGMEVSGYDENMNTIRTYOVCHVFESSQNNMLR 60
 23 LLAVEETLMDSTTATATLGMVHPPSGMEVSGYDENMNTIRTYOVCHVFESSQNNMLR 82
 61 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYYEADPDSATKTPNNMEMP 120
 83 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYYEADPDLATKTPNNMEMP 142
 121 WKVYDTIAADESFQVLDGGRVMIINTEVRSFGVSRSGFYLAFODYGGCMLIAVVFY 180
 143 WKVYDTIAADESFQVLDGGRVMIINTEVRSFGVSRSGFYLAFODYGGCMLIAVVFY 202
 181 RKCPRILIONGALIFDETLGSAESTSLVAARGSCINAAEEVDVPIKLYCNGDEMLVPIGRC 240
 203 RKCPRILIONGALIFDETLGSAESTSLVAARGSCINAAEEVDVPIKLYCNGDEMLVPIGRC 262
 241 MCKAFEEVENGTGRCGPGSGTFKANKOGDEACTHCPINSRTTSEGATNCVCRNGYYRADL 300
 263 MCKAFEEVENGTGRCGPGSGTFKANKOGDEACTHCPINSRTTSEGATNCVCRNGYYRADL 322
 301 DPLDMPCTTIPSAPOAVISVNETSLMLEWTPPRDSGGREDLVYMIICKSGSGGACTR 360
 323 DPLDMPCTTIPSAPOAVISVNETSLMLEWTPPRDSGGREDLVYMIICKSGSGGACTR 382
 361 CGDNVOYARROUGLTERPRITISDLAHTQYTFEIOAVNCGVTDOSPFQFASVNTITNQA 420
 383 CGDNVOYARROUGLTERPRITISDLAHTQYTFEIOAVNCGVTDOSPFQFASVNTITNQA 442

421 APSAVSIMHOVSRTVDSTITLSMSPDPDPNGVILDELYEQLYKEKISEYNATAIKSPNTVT 480
 443 APSAVSIMHOVSRTVDSTITLSMSPDPDPNGVILDELYEQLYKEKISEYNATAIKSPNTVT 502
 481 --GLKAGAIYQVVARFVAGYGRYSGKMYFQTMTEABYQISIOEKPLIIGSSAGAGVF 538
 503 VQGLKAGAIYQVVARFVAGYGRYSGKMYFQTMTEABYQISIOEKPLIIGSSAGAGVF 562

539 LIAVVVIAI 547
 563 LIAVVVIAI 571

RESULT 9
 US-09-621-595-2
 Sequence 2, Application US/09621595
 GENERAL INFORMATION:
 APPLICANT: Pawson, Anthony
 TITLE OF INVENTION: Method of Activating a Novel Ligand
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Room 970
 STREET: 600 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1X5

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/621,595
 FILING DATE: 21-Jul-2000
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/730,700
 FILING DATE: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydyk, Linda M.
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-196
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 416-586-3235
 TELEFAX: 416-586-3110
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 994 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-621-595-2

Query Match 99.1%; Score 2870; DB 20; Length 994;
 Best Local Similarity 98.9%; Pred. No. 5.7e-259;
 Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

1 LLAVEETLMDSTTATATLGMVHPPSGMEVSGYDENMNTIRTYOVCHVFESSQNNMLR 60
 23 LLAVEETLMDSTTATATLGMVHPPSGMEVSGYDENMNTIRTYOVCHVFESSQNNMLR 82
 61 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYYEADPDSATKTPNNMEMP 120
 83 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYYEADPDLATKTPNNMEMP 142
 121 WKVYDTIAADESFQVLDGGRVMIINTEVRSFGVSRSGFYLAFODYGGCMLIAVVFY 180

```

Db 143 WKVVTIADESESQVDLGRVAKINTFEVRSRGVPSRNGFYLAFODYGCMSLIAVRFY 202
OY 181 RKCPTIIONGAFEOETLSGAESTSLVAAAGSCIANAEVDVPIKLYCNGDEMLVPIGR 240
Db 203 RKCPTIIONGAFEOETLSGAESTSLVAAAGSCIANAEVDVPIKLYCNGDEMLVPIGR 262
OY 241 MCKAFEAVENTGTCRGCPSTGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGYRADL 300
Db 263 MCKAFEAVENTGTCRGCPSTGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGYRADL 322
OY 301 DPLDMPCCTTISAPQAVISSVNETSLMLEMPPRDSGREDLVNITCKSCGSGGACTR 360
Db 323 DPLDMPCCTTISAPQAVISSVNETSLMLEMPPRDSGREDLVNITCKSCGSGGACTR 382
OY 361 CGDNQVAPROLGLTEPRITISDLAHTQYFEIOAVNGVTDOSPSPOPASVNTTMOA 420
Db 383 CGDNQVAPROLGLTEPRITISDLAHTQYFEIOAVNGVTDOSPSPOPASVNTTMOA 442
OY 421 APSAVSIMHOVSRTVDSITLMSQPDQPNVILDELOYEKELESEYNATAIKSPTNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLMSQPDQPNVILDELOYEKELESEYNATAIKSPTNTVT 502
OY 481 --GLKAGAIYFOVARVAVGYGRSGKMYFOTMTEAEYQTSIQEKLPLITGSSAGLVF 538
Db 503 VQGLAGAIYFOVARVAVGYGRSGKMYFOTMTEAEYQTSIQEKLPLITGSSAGLVF 562
OY 539 LIAVVVIAI 547
Db 563 LIAVVVIAI 571

RESULT 10
US-09-194-755A-7
: Sequence 7, Application US/09194755A
: GENERAL INFORMATION:
: APPLICANT: Matsui, Toshimitsu
: TITLE OF INVENTION: Novel Human Receptor Type Tyrosine
: TITLE OF INVENTION: Kinases Like Protein
: FILE REFERENCE: 07541.0001-00000
: CURRENT APPLICATION NUMBER: US/09/194,755A
: PRIOR FILING DATE: 1999-04-14
: PRIOR APPLICATION NUMBER: PCT/JP97/01867
: PRIOR FILING DATE: 1997-06-04
: PRIOR APPLICATION NUMBER: JP 141849/1996
: PRIOR FILING DATE: 1996-06-04
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 7
: LENGTH: 990
: TYPE: PRT
: ORGANISM: Rattus sp.
US-09-194-755A-7

```

```

Query Match 71.8%; Score 2078.5; DB 15; Length 990;
Best Local Similarity 67.9%; Pred. No. 8,7e-185;
Matches 376; Conservative 86; Mismatches 83; Indels 9; Gaps 3;

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```

OY 2 LAAVEETLMDSTTATAEELGMVHP-PSGMEVSGYDENMNTIRTYOVNVESSONNLRT 61
Db 15 VAAAEETLMDTTRTATLGTANPASWHEVSGYDENMNTIRTYOVNVESSONNLRT 74
OY 62 KPIRRGAHRIHWEKPSVBDSCSIPSPGCKETENLYYYEADFDSATKTFPMENPM 121
Db 75 TFIIRGAHRIYTEMRTVDCSLPNVPGCKETENLYYYEADFDSATKTFPMENPM 134
OY 122 VXYDTIADDSFS-----QVDLGRVAKINTFEVRSRGVPSRNGFYLAFODYGCMSLIA 175
Db 135 LKVDITIADESFSSSSAAMQVDFGGRILMKVNTVEYRSGPLTRNGFYLAFODYGCMSLIS 194
OY 176 VVFEYRKCPSTIIONGAFEOETLSGAESTSLVAAAGSCIANAEVDVPIKLYCNGDEMLV 235
Db 199 VVFEYRKCPSTIIONGAFEOETLSGAESTSLVAAAGSCIANAEVDVPIKLYCNGDEMLV 254

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Db 195 VVFEYRKCPSTIIONGAFEOETLSGAESTSLVIAAGTCIPNAEVDVPIKLYCNGDEMLV 254
OY 236 PIGRCMKAFEAVENTGTCRGCPSTGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGY 295
Db 255 PIGRCMKAFEAVENTGTCRGCPSTGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGY 313
OY 296 YRADLDPLEDMPCCTTISAPQAVISSVNETSLMLEMPPRDSGREDLVNITCKSCGSGR 355
Db 314 YRADLDPLEDMPCCTTISAPQAVISSVNETSLMLEMPPRDSGREDLVNITCKSCGSGR 373
OY 356 GACTRCGDNQVAPROLGLTEPRITISDLAHTQYFEIOAVNGVTDOSPSPOPASVNI 415
Db 374 RSCRCDDNVAFVPRQGLTECRVSSISLMHTPTTDIAQINVSRSKSPRPOHVSNI 433
OY 416 TTNQAAPSTVPIHVOVSATMNSITLSPPOPNGLIIDEIRYEREKHEHFNSSMARSO 493
Db 434 TTNQAAPSTVPIHVOVSATMNSITLSPPOPNGLIIDEIRYEREKHEHFNSSMARSO 493
OY 476 TTNQAAPSTVPIHVOVSATMNSITLSPPOPNGLIIDEIRYEREKHEHFNSSMARSO 493
Db 494 TTNQAAPSTVPIHVOVSATMNSITLSPPOPNGLIIDEIRYEREKHEHFNSSMARSO 493
OY 534 AGVFEVVSIVAISI 567
Db 554 AGVFEVVSIVAISI 567

```

```

RESULT 11
US-07-861-390D-6
: Sequence 6, Application US/07861390D
: GENERAL INFORMATION:
: APPLICANT: PAMSON et al.
: TITLE OF INVENTION: METHOD FOR EXPRESSING A
: TITLE OF INVENTION: PHOSPHORYLATED PROTEIN
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Linda M. Kurdzyk, Bereskin & Parr
: STREET: 40 King Street West, P. O. Box 401
: CITY: Toronto, Ontario
: STATE: N/A
: COUNTRY: Canada
: ZIP: M5H 3Y2
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: DOS Text File
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/861,390D
: FILING DATE: 19920331
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: J.G. Mullins
: REGISTRATION NUMBER: 33073
: REFERENCE/DOCKET NUMBER: 027-021
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 684-1111
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1009 amino acids
: TYPE: AMINO ACIDS
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-07-861-390D-6

```

```

Query Match 68.3%; Score 1976; DB 3; Length 1009;
Best Local Similarity 66.0%; Pred. No. 3.6e-175;
Matches 371; Conservative 86; Mismatches 89; Indels 16; Gaps 10;
OY 2 LAAVEETLMDSTTATAEELGMVHP-PSGMEVSGYDENMNTIRTYOVNVESSONNLRT 59
Db 199 VVFEYRKCPSTIIONGAFEOETLSGAESTSLVAAAGSCIANAEVDVPIKLYCNGDEMLV 254

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Db 15 VAAMEITLMDTRATATLGTWAMPXASGMEVSGYDENLNTIRTYQVCNXYFEPNOMNL 74
OY RTKTRRRG-AARIHVEKFSVRDCCSIPSP--GSCKEFNLYYEADFSATKTFPNM 116
75 LTTFINRGAXHRIYETMRFTVROCCSLPNVPXKSGCKETFNLYYETDVIATKKSAM 134
OY 117 MENPVAVDTIADESQVDLGRVAKINTEVRSFGVPSGFGYLAQDYGCCSLIAY 176
135 SEAPLKVDIIAIDSEFSQVDFGRLMKVTEVRSFGPLTRNGFYLAQDYGACMSLLSY 194
OY 177 RVEYKCRITIOGAIPEQETLSGASTSLVARGSCIANAEVDVP---IKLYCGDGM 233
195 RVEFKCSIVQNFVPELIMGASTSLVARGTCIPNAEVDVPXKIKLYCGDGM 254
OY 234 LVPTGCMKAGFEAVENGTCRGCPSGTFKANOGEACTHCPINSRTTSEGATNCVCRN 293
255 MYPICRCCKAGPEPENSXVACKACPACTFKASQBEAGCSHCPSNRSSEASPICCTRT 314
OY 294 GYRADLPDMPCCTTISAPQAVISSV-NETSLEMTPPRDSGREDLVYNIICKSCG 352
315 GYRADFPPEPACTSVSPGPNVISTYXNETSILEMHPRETGGRDVTYNIICKCX 374
OY 353 SGRG---ACTRCGDVVOYAPROLGLEPRITYISDLAHTQYTFEIOAVNGVTDSPSPQ 409
375 XKRADRRSGSCDDNVEFVPROLGLTECVSISLMAHTPYFDIOLINGVSKSPFPQ 434
OY 410 -FASVNTTNOAPSASVIMHO-VSRFYDSTLSWSQDPQNGVILIDYLOYEKELSEY 467
435 HVXSVNTTNOAPSASVIMHO-VSRFYDSTLSWSQDPQNGVILIDYLOYEKELSEY 494
OY 468 NATALKSPNT--VTGLKGAIVYFOVARTAVAGRYSGKMYFQMTAEFOTSIQEL 525
495 NSSMARSOITNRIKIDLRGAWYVVOVRAIRYAGIKCFSGKMCFOITDDDKSELREGL 554
OY 526 PLIGSSAGLVELIAVVYIAI 547
555 PLIGSSAGLVELIAVVYIAI 576
Db 555 PLIGSSAGLVELIAVVYIAI 576

RESULT 12
; Sequence 20, Application US/08449645
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; APPLICANT: Melcher, Andrew A.
; APPLICANT: Juing, Shuguan
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaviiland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645
; FILING DATE: May 24, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287-A
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645-20

Query Match 62.2%; Score 1800.5; DB 8; Length 998;
Best Local Similarity 61.9%; Pred. No. 1e-158;
Matches 340; Conservative 79; Mismatches 119; Gaps 5;

OY 4 AVEETLMDSTATATLGMVHPSPGMEVSGYDENLNTIRTYQVCNXYFEPNOMNLTRKF 63
177 RVEYKCRITIOGAIPEQETLSGASTSLVARGSCIANAEVDVP---IKLYCGDGM 233
195 RVEFKCSIVQNFVPELIMGASTSLVARGTCIPNAEVDVPXKIKLYCGDGM 254
OY 234 LVPTGCMKAGFEAVENGTCRGCPSGTFKANOGEACTHCPINSRTTSEGATNCVCRN 293
255 MYPICRCCKAGPEPENSXVACKACPACTFKASQBEAGCSHCPSNRSSEASPICCTRT 314
OY 294 GYRADLPDMPCCTTISAPQAVISSV-NETSLEMTPPRDSGREDLVYNIICKSCG 352
315 GYRADFPPEPACTSVSPGPNVISTYXNETSILEMHPRETGGRDVTYNIICKCX 374
OY 353 SGRG---ACTRCGDVVOYAPROLGLEPRITYISDLAHTQYTFEIOAVNGVTDSPSPQ 409
375 XKRADRRSGSCDDNVEFVPROLGLTECVSISLMAHTPYFDIOLINGVSKSPFPQ 434
OY 410 -FASVNTTNOAPSASVIMHO-VSRFYDSTLSWSQDPQNGVILIDYLOYEKELSEY 467
435 HVXSVNTTNOAPSASVIMHO-VSRFYDSTLSWSQDPQNGVILIDYLOYEKELSEY 494
OY 468 NATALKSPNT--VTGLKGAIVYFOVARTAVAGRYSGKMYFQMTAEFOTSIQEL 525
495 NSSMARSOITNRIKIDLRGAWYVVOVRAIRYAGIKCFSGKMCFOITDDDKSELREGL 554
OY 526 PLIGSSAGLVELIAVVYIAI 547
555 PLIGSSAGLVELIAVVYIAI 576
Db 555 PLIGSSAGLVELIAVVYIAI 576

RESULT 13
; Sequence 20, Application US/08702367
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; APPLICANT: Juing, Shuguan
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaviiland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367
; FILING DATE:

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,509
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367-20

Query Match 62.2% Score 1800.5; DB 11; Length 998;
Best Local Similarity 61.9%; Pred. No. 1e-158;
Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYOVGNVPESSONMLRTKF 63
DB 37 ALEETLMDTKWTSLELATMSHESGMEVSGYDEAMNPIRTYOVGNVPESSONMLRTGF 96
QY 64 IRRGAHRHVMKTSVDCSSIPSPGCKETENLYYEADFSATKTPNMENPVK 123
DB 97 IMRQVORVYELKFTVRCNSIPNIPGCKETENLYYEADFSATKTPNMENPVK 156
QY 124 VDTIADSEFSQVDLGGVYMKINTEVRSFGVSRGFLAFODYGGCMLAVAVFYKRC 183
DB 157 VDTIADSEFSRLDAG---RVNTKVRSGFLSKAGFLAFODYGGCMLAVAVFYKRC 212
QY 184 PRIIONGAIFQETLSGASTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRCK 243
DB 213 ASTAGFALFPEETLTGAEPSTLVIAFGTCIPNAVEVSVPKLYCNGDGEMLVPIGRCK 272
QY 244 AGFEAVENGTVRCGPGSTGFRKANGDEACTHCPTNSRTSGATNCVCRNGYRADIDPL 303
DB 273 TGHPEAKESQCRCPSPSTYAKOGEGPCLPSPNSRTSPAAISICCHNNFYRADSDA 332
QY 304 DMCPTTIPSAQVAISSVNETSLMLEWTPPRDSGREDLVYNIICKSC--GSGRGAQTRC 361
DB 333 DSACTVPSPRGVISNVNETSLILEMSEPRDLGVRDLLYNIICKCHGAGGASACSRC 392
QY 362 GDNVOYAPROLGLTEPRYISDLAHTQYTFEIOAVNGVTDOSPFSPQFASVNTTNOAA 421
DB 393 DDNVEFVRQLGSEPRVHTSHLAHRTYFEVQAVNGVSGKSPLPFRVAAVNTTNOAA 452
QY 422 PSAVISIMHQSRTVDSITLMSQDPDOPNGVILDELOYKEKELSEYNATAIKSPNTV-- 479
DB 453 PSEVPTLRHSSSGSSSLTMSAPPERNGVILDELOYKEKELSEYNATAIKSPNTV-- 510
QY 480 TGLKAGAIYVOVARTVAGYGRYSGKMYFQYMT--AEYTSIOEKPLITIGSSAAGLV 538
DB 511 DGLRPDARIYVOVARTVAGYGRYSGKMYFQYMT--AEYTSIOEKPLITIGSSAAGLV 570
QY 539 LIAVVYIAI 547
DB 571 VVAVVYIAI 579

RESULT 14
US-09-378-759-20
Sequence 20, Application US/09378759
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehaven Drive

CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,759
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-378-759-20

Query Match 62.2% Score 1800.5; DB 17; Length 998;
Best Local Similarity 61.9%; Pred. No. 1e-158;
Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYOVGNVPESSONMLRTKF 63
DB 37 ALEETLMDTKWTSLELATMSHESGMEVSGYDEAMNPIRTYOVGNVPESSONMLRTGF 96
QY 64 IRRGAHRHVMKTSVDCSSIPSPGCKETENLYYEADFSATKTPNMENPVK 123
DB 97 IMRQVORVYELKFTVRCNSIPNIPGCKETENLYYEADFSATKTPNMENPVK 156
QY 124 VDTIADSEFSQVDLGGVYMKINTEVRSFGVSRGFLAFODYGGCMLAVAVFYKRC 183
DB 157 VDTIADSEFSRLDAG---RVNTKVRSGFLSKAGFLAFODYGGCMLAVAVFYKRC 212
QY 184 PRIIONGAIFQETLSGASTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRCK 243
DB 213 ASTAGFALFPEETLTGAEPSTLVIAFGTCIPNAVEVSVPKLYCNGDGEMLVPIGRCK 272
QY 244 AGFEAVENGTVRCGPGSTGFRKANGDEACTHCPTNSRTSGATNCVCRNGYRADIDPL 303
DB 273 TGHPEAKESQCRCPSPSTYAKOGEGPCLPSPNSRTSPAAISICCHNNFYRADSDA 332
QY 304 DMCPTTIPSAQVAISSVNETSLMLEWTPPRDSGREDLVYNIICKSC--GSGRGAQTRC 361
DB 333 DSACTVPSPRGVISNVNETSLILEMSEPRDLGVRDLLYNIICKCHGAGGASACSRC 392
QY 362 GDNVOYAPROLGLTEPRYISDLAHTQYTFEIOAVNGVTDOSPFSPQFASVNTTNOAA 421
DB 393 DDNVEFVRQLGSEPRVHTSHLAHRTYFEVQAVNGVSGKSPLPFRVAAVNTTNOAA 452
QY 422 PSAVISIMHQSRTVDSITLMSQDPDOPNGVILDELOYKEKELSEYNATAIKSPNTV-- 479
DB 453 PSEVPTLRHSSSGSSSLTMSAPPERNGVILDELOYKEKELSEYNATAIKSPNTV-- 510
QY 480 TGLKAGAIYVOVARTVAGYGRYSGKMYFQYMT--AEYTSIOEKPLITIGSSAAGLV 538
DB 511 DGLRPDARIYVOVARTVAGYGRYSGKMYFQYMT--AEYTSIOEKPLITIGSSAAGLV 570
QY 539 LIAVVYIAI 547
DB 571 VVAVVYIAI 579

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RESULT 15
PCT-US01-03800A-2273
; Sequence 2273, Application PC/TUS0103800A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: PCT/US01/03800A
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2273
; LENGTH: 1007
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03800A-2273

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Query Match 62.2%; Score 1800.5; DB 1; Length 1007;
Best Local Similarity 61.9%; Pred. No. 1e-158;
Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTTAAELGMMVHPSPGWEVSGYDENNTIRTYQVCNVFESSQNNMLRTKF 63
DB 46 ALEETLMDTKWVTSLELAWSHPESGWEVSGYDEANMPIRTYQVCNVRESSQNNMLRTGF 105
QY 64 IRRRGARHIVENKFSVRDCSSIPSVGSKETFNLYYEADPDSATKTFPMNMENPVWK 123
DB 106 IMRDRQRYVELKFTYVDCNSIPNIPGSKETFNLYYEADSDVASASSPFMMENPVWK 165
QY 124 VDTIADDESQVDLGRWKKINTEVRSFGVRSFGFYLAFOYGGCMSLIAVRYRKC 183
DB 166 VDTIADDESQVDLGRWKKINTEVRSFGVRSFGFYLAFOYGGCMSLIAVRYRKC 221
QY 184 PRITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCK 243
DB 222 ASITAGALPELTIGNEPISLVAPCTCIPNAVEVSVPLKLYCNGDGEWLVPIGRCK 281
QY 244 AGPEAVENGVCRCGCEGTAKANGDEACTHCPIINSRTSEGATNCVCRNGYRADIDPL 303
DB 282 TGHEPAKESQCRCPGSKAKQGBECPCLPCPNKRTTSPASISICTCHNNFYRADSDA 341
QY 304 DMPCTTIPSAPOAVISSVNETSLMELTPPRDSGGRDLVYNIICKSC--GSGRACATRC 361
DB 342 DSACTTVPSPRGVYSNVNETSLILEMSEPRDLGVDDLLYNVICKKHGAGGASACSRC 401
QY 362 GDNVQYAPRQGLTEPRIYISDLAHTQYFEIOAVNGVTDQSPFPOFASVNTTNOAA 421
DB 402 DDNEFEVPRQGLSEPRVHTSHLAHTRYFEVQAVNGVSGKSPLPPIRYAVANTTNOAA 461
QY 422 PSVSIHQVSRVDTSLISQDOPDNGVTLDELOYEKELESEYNATAIKSPNTV-- 479
DB 462 PSEVPPTLRHSSSSSLTSLSWAPPERNGVLLDYEKTFEK--SEGIASTYTGQMSVOL 519
QY 480 TGLKAGAIYVFOVARIVAGYGRYSGKMYEQTME-AYQTSIQEKLPLIIGSSAGLVF 538
DB 520 DGLRPDAIYVFOVARIVAGYGRYSGKMYEQTME-AYQTSIQEKLPLIIGSSAGLVF 579
QY 539 LIAVVVIAI 547
DB 580 VVAVVVIAI 588

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 1, 2002, 10:00:07 ; Search time 26.14 Seconds
(without alignments)
874.598 Million cell updates/sec

Title: US-09-378-759-11_COPY_1_547
Perfect score: 2895
Sequence: 1 LIAVETLMDSTTATFALG.....ITGSSAAGLVEFLIAVVVIAL 547

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 202503 seqs, 41795235 residues

Total number of hits satisfying chosen parameters: 202503

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New: *
1: /cgn2_6/ptodata/1/paa/PCN_NEW_COMB.pep: *
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep: *
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep: *
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep: *
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep: *
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep: *
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2083.5	72.0	984	7	US-60-341-631-3
2	1485.5	51.3	1037	7	US-60-339-995-3
3	1414	48.8	942	6	US-10-004-542-2
4	1410	48.7	1036	5	US-09-971-708-2
5	1410	48.7	1130	5	US-09-922-138-2
6	1395	48.2	1035	5	US-09-971-708-3
7	784.5	27.1	265	1	PCN-US01-30539-4
8	783.5	27.1	265	1	PCN-US01-30539-5
9	783.5	27.1	265	1	PCN-US01-30539-6
10	686	23.4	295	1	PCN-US01-30539-2
11	678	23.4	178	5	US-09-922-138-10
12	666.5	23.0	180	5	US-09-922-138-12
13	531.5	18.4	180	5	US-09-922-138-15
14	429.5	14.8	127	5	US-09-922-138-13
15	405	14.0	116	6	US-10-029-386-33374
16	341.5	11.8	116	6	US-10-029-386-32097
17	200	6.0	59	5	US-09-922-138-15
18	174.5	6.0	1518	7	US-60-340-187-384
19	174	6.0	1461	5	US-09-976-594-531
20	158.5	5.3	5701	6	US-10-029-386-32438
21	153	5.3	760	5	US-09-611-526-3462
22	149	5.1	1382	5	US-09-971-873-7
23	148	5.1	1351	5	US-09-970-318-4
24	146.5	5.1	1948	5	US-09-800-198-45
25	144	5.0	595	6	US-10-029-386-32978
26	143.5	5.0	980	5	US-09-908-193-22

27	140.5	4.9	588	6	US-10-029-386-33963	Sequence 33963, A
28	140	4.8	1502	5	US-09-800-198-44	Sequence 44, Appl
29	136.5	4.7	1252	5	US-09-908-193-21	Sequence 21, Appl
30	135.5	4.7	1252	5	US-10-029-386-32098	Sequence 32098, A
31	135	4.7	1247	5	US-09-908-193-2	Sequence 2, Appl
32	134.5	4.6	1252	5	US-09-908-193-19	Sequence 19, Appl
33	134.5	4.6	1253	5	US-09-908-193-20	Sequence 20, Appl
34	131	4.5	1008	5	US-09-908-193-11	Sequence 11, Appl
35	126	4.4	886	5	US-09-923-559-11	Sequence 57, Appl
36	125.5	4.3	2012	5	US-09-922-647-11	Sequence 5, Appl
37	120	4.1	468	5	US-09-800-198-57	Sequence 55, Appl
38	119.5	4.1	1375	5	US-09-950-149-5	Sequence 27, Appl
39	118	4.1	1260	6	US-09-800-198-55	Sequence 2857, Ap
40	117.5	4.1	570	5	US-10-024-918-27	Sequence 103, Ap
41	116	4.0	1138	6	US-10-021-660-101	Sequence 113, App
42	116	4.0	1786	5	US-09-873-676-113	Sequence 61, Appl
43	115.5	4.0	2167	5	US-09-778-927A-61	Sequence 2, Appl
44	115	4.0	1107	5	US-09-977-053-2	
45	115	4.0	1395	5	US-09-800-198-56	Sequence 56, Appl

ALIGNMENTS

```
RESULT 1
US-60-341-631-3
; Sequence 3, Application US/60341631
; GENERAL INFORMATION:
; APPLICANT: Spallmann, Frank
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1421 AND 14381
; FILE REFERENCE: MP12001-293PI(M)
; CURRENT APPLICATION NUMBER: US/60/341.631
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Homo Sapien
US-60-341-631-3
```

Query Match Best Local Similarity 72.0% Score 2083.5; DB 7; Length 984;
Matches 374; Conservative 87; Mismatches 84; Indels 3; Gaps 2;

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QY 2 LAVETLMDSTTATFALGMMVHPSPGMEVSGYDENMTTFTYQVNCVNFESSQNMKLT 61
D 15 VAAWETLMDTRTATFALGMMVHPSPGMEVSGYDENMTTFTYQVNCVNFESSQNMKLT 74
QY 62 KPIRRGRRHRIHVEKRSVRCSSIPSPGCKETFMILYYEADFDSATKTFPPNMENPM 121
D 75 TFINRGRRHRIHVEKRSVRCSSIPSPGCKETFMILYYEADFDSATKTFPPNMENPM 134
QY 122 VKVDITIADESFQVDDGGRVMTKTEVRSGPVSRCGFYLAODVGGGSLAAYRFT 181
D 135 LKVDITIADESFQVDDGGRVMTKTEVRSGPVSRCGFYLAODVGGGSLAAYRFT 194
QY 182 KCPRIIONGALFOTLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRM 241
D 195 KCPRIIONGALFOTLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRM 254
QY 242 CKAGFEVNGTVCRCGPGSTFRKANGDEACTHCPINSRTSGATNCVCRNGYRADID 301
D 255 CKAGFEVNGTVCRCGPGSTFRKANGDEACTHCPINSRTSGATNCVCRNGYRADID 313
QY 302 PLMDPCTTISAPQAVISSVNETSLMLEWTTPRDSGGRDLVYNIICKSGSGRACTRC 361
D 314 PPEVACTSVPSGGRNVISIVNETSILEWHPPRETGGRDVTYNIICKSGSGRACTRC 373
QY 362 GDMVQYARQLGLTEPRRIYISDLAHTQYTFELQAVNGVTDGSPSPQFASVNTTNOA 421
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Db 374 DDNEVEPRQGLTECKRSISLWHPYTFDIOAINGVSSKSPFPQHVSVNTTNOAA 433
OY 422 PSASIMHQSRTVDSITLWSOPDQNGVILDYELQYKEKLSYNAITAIRSTNT--V 479
Db 434 PSTVIMHQSRTVDSITLWSOPDQNGVILDYELQYKEKLSYNAITAIRSTNTARI 493
OY 480 TGLKGAIVYQVARTVAGYGRYSKMYFOTMTAEYQTSIOEKPLITIGSSAGLVFL 539
Db 494 DGLRGMYVVOVARTVAGYGRYSKMYFOTMTAEYQTSIOEKPLITIGSSAGLVFL 553
OY 540 IAVVIAI 547
Db 554 VSLVAISI 561

RESULT 2
US-60-339-995-3
; Sequence 3, Application US/60339995
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Mayoung
; TITLE OF INVENTION: Methods and Compositions to Treat
; TITLE OF INVENTION: Cardiovascular Disease Using 1419, 58765 and 2210
; FILE REFERENCE: MP12001-291P1(M)
; CURRENT APPLICATION NUMBER: US/60/339,995
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: PRF
; ORGANISM: Homo Sapien
US-60-339-995-3

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Query Match 51.3%; Score 1485.5; DB 7; Length 1037;
Best Local Similarity 50.7%; Pred. No. 4.3e-119; Indels 11; Gaps 7;
Matches 276; Conservative 107; Mismatches 150;

```

```

OY 6 EETLMDSTTAAELGMMVHPSPGMEVSGYDENMNTIRTYOVCAVPESSONMLRTKFR 65
Db 60 EVNLIDRTVAGDGLWIAFPKNGMEIGEVDEYAPRHTYOVCAVPESSONMLRTKFR 119
OY 66 RGAHRIHVEKESVRCDSIPVSGCKETFNLYYEADPDSATKTFPMMEPNWYKVD 125
Db 120 NEGASRIETELKFTLRDONSIPGIGTCKETFNMYFESDDQNGR---NIKENQIKID 175
OY 126 TTADESFOVDLGRVWKINTYEVRSFGPVSRSGFYLAFOYGGMSLIAVRYFKCPR 185
Db 176 TTADESFOVDLGRVWKINTYEVRSFGPVSRSGFYLAFOYGGMSLIAVRYFKCPS 235
OY 186 ITONGAIFQETLSGAESTSLVAARSCIANAEVDVPIKLYCNGDEMLVPIGRCKAG 245
Db 236 VYRHIAVPRDITGADSQLLEVSGCV-NHNVDEPKMKCSAEGEWLVPIGRCKAG 294
OY 246 FEAVANGVCGCPSTGKANOGEACHTCPINSRTTSGATNCVCRNGYRADLDPLDM 305
Db 295 YEE-RNGT-CQVCRPGFTRKASHIOCKCPPHSTTHEATSCVCEKDEYRRRSDPPTM 352
OY 306 PCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSGSGRACRRCGNV 365
Db 353 ACTRPPSAPRNAMISWNESVLEWIPRADTGGKRDVSYIACKNCNSHAGVCEEGGHV 412
OY 366 QYAPROLGTEPRITISDLAHTOYTFELQAVNGVTDOSPSPORASVNTTNOAASAV 425
Db 413 RYLPKROSGKNTSYMWVLDLAFNTFTLEAVNGVSDLSFGARQYVSVNTTNOAASAV 472
OY 426 STMHQVSRVDSITLWSOPDQNGVILDYELQYKEKLSYNAITAIRSTNT--GLK 483
Db 473 TAVKAKIKAKNSISLWSOPDQNGVILDYELQYKEKLSYNAITAIRSTNT--GLK 531
OY 484 AGAIVYQVARTVAGYGRYSKMYFOTMTAEYQTSIOEKPLITIGSSAGLVFLAVI 543

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Db 532 PASVYFQIRARTVAGYGRYSKMYFOTMTAEYQTSIOEKPLITIGSSAGLVFLAVI 590
OY 544 VIAI 547
Db 591 GVLL 594

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RESULT 3
US-10-004-542-2
; Sequence 2, Application US/10004542
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Walke, D. Wade
; APPLICANT: Fiddie, Carl Johan
; TITLE OF INVENTION: Novel Human Kinase and Polynucleotides
; FILE REFERENCE: Lex-0260-USA
; CURRENT APPLICATION NUMBER: US/10/004,542
; PRIOR FILING DATE: 2001-10-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 942
; TYPE: PRF
; ORGANISM: homo sapiens
US-10-004-542-2

```

```

Query Match 48.8%; Score 1414; DB 6; Length 942;
Best Local Similarity 48.1%; Pred. No. 5.2e-113; Indels 12; Gaps 7;
Matches 260; Conservative 106; Mismatches 162;

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OY 9 LMDSTTAAELGMMVHPSPGMEVSGYDENMNTIRTYOVCAVPESSONMLRTKFR 68
Db 131 LMDSTTAAELGMMVHPSPGMEVSGYDENMNTIRTYOVCAVPESSONMLRTKFR 190
OY 69 ARIHVEKESVRCDSIPVSGCKETFNLYYEADPDSATKTFPMMEPNWYKVD 128
Db 191 ARIHVEKESVRCDSIPVSGCKETFNLYYEADPDSATKTFPMMEPNWYKVD 246
OY 129 ADESFQVDLGRVWKINTYEVRSFGPVSRSGFYLAFOYGGMSLIAVRYFKCPR 188
Db 247 ADESFQVDLGRVWKINTYEVRSFGPVSRSGFYLAFOYGGMSLIAVRYFKCPR 306
OY 189 NGAIPOETLSGAESTSLVAARSCIANAEVDVPIKLYCNGDEMLVPIGRCKAG 248
Db 307 NLAEPDITPRDSSSLVARSCKVSAERDLP-KLVCGADGDMVLPGRICSTGYEE 365
OY 249 VENGTVRCGCPSTGKANOGEACHTCPINSRTTSGATNCVCRNGYRADLDPLDM 308
Db 366 IEGS--CHACRPFYKAFAGNTRKSCPCPHSLTYMDATSVCCGEGYFAEKDPSPMACT 423
OY 309 TITSAPQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSGSGRACRRCGNV 368
Db 424 RPPSAPRNAMISWNESVLEWIPRADTGGKRDVSYIACKNCNSHAGVCEEGGHV 483
OY 369 PROGLTEPRITISDLAHTOYTFELQAVNGVTDOSPSPORASVNTTNOAASAV 427
Db 484 PRHGLINNVTIYLDVDFSHVNTYFEIEMANGVSELS-FSPKPELATVTTDDADPSLIGV 542
OY 428 MHQVSRVDSITLWSOPDQNGVILDYELQYKEKLSYNAITAIRSTNT--YNAITAIRSTNT 485
Db 543 VRKMAQONSIALSWQPARSNGAILDYELQYKEKLSYNAITAIRSTNT--YNAITAIRSTNT 602
OY 486 AIVYQVARTVAGYGRYSKMYFOTMTAEYQTSIOEKPLITIGSSAGLVFLAVI 545
Db 603 TKYFHRIRVARTVAGYGRYSKMYFOTMTAEYQTSIOEKPLITIGSSAGLVFLAVI 661

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RESULT 4
US-09-971-708-2
; Sequence 2, Application US/09971708
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Human EphA6 Gene and Polypeptide
; FILE REFERENCE: OGT 16U 102 R1
; CURRENT APPLICATION NUMBER: US/09/971,708
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-971-708-2

```

```

Query Match          48.7%; Score 1410; DB 5; Length 1036;
Best Local Similarity 48.0%; Pred. No. 1.3e-112;
Matches 259; Conservative 106; Mismatches 163; Indels 12; Gaps 7;

```

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QY 9 LMDSTATAELGMVHPSPGMEVSGYDENMNTITRTYQCNVFESSONNMLTRKRRRG 68
D 131 LDDTTVLGELGKRTYPLNGMDATTEMDENRPIHTYQCNVMEPNONNMTRNWSRDA 96
QY 69 AHRHVEKRSVRCSSIPSPGCKETFNLYYEADFSATRTFPMNMPVVKYDTIA 128
D 191 AOKIYEMKFTLRDCNSIPWVLGCTKETFNLFYMESESHGKFRP----NOYTKIDTIA 152
QY 129 ADEFSQVDLGRVAKINTFVRSRSGFYLAFOYGGCMSLIAVRYFKCRPIIQ 188
D 153 ADESTQMDLGRILKNTREVGPIERKGFYLAFODIGACIALVSRYFYKCCPFYVR 212
QY 189 NGAIQETLSGAESTSLVAARGSCIANAEEDVPRIKLYCNGDEWLPIGRCKAKGFEA 248
D 213 NLAMPPTIRPVSSSLVEVRGSCVKSABERDTP-KLYCGADMDLVPILGRICSTGYEE 271
QY 249 VENGTVGCGSGTFRKANOGDEACTHCPINRRTSGATNCVCRNGYRADLPLDMPCT 308
D 272 IEGS--CHACRPFFYAFAGNTKSCPCPSHSLTYMEATSVCCCKEYFAAEKDPMSMACT 329
QY 309 TTPSAPQAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSGSGRACRCGDVVOYA 368
D 330 RPPSAPRVNVEFINETALLIEMSPSDTGKRDLYSVICKKCGLDTSQCECCGGGLRPI 389
QY 369 PROGLTEPRITYSDLAHQVTFEIOAVNGVTDQSPSPQ--FASVNTTNOAPSASVI 427
D 390 PRHTGLINNSVIVLDFVSHVNTFEIEMNGVSELS-FSPKPFRTIYVTTDDAPSLIGV 448
QY 428 MQVSRVDSITLSMSQPDOPNGVILDELOYEKEKELSE--YNATAIKSPNTVYGLKAG 485
D 449 VRKQWASQNSIALSMQAPAFNSGAILDYEIKIYKEKEHEGLTSSRSKAPSVITIGLPA 508
QY 486 AIYVFOVARTVAGYGRYSGKMYFQTMTEAEYQTSIOEKPLIIGSSAAGLVFLAVVVI 545
D 509 TKYVFHIRVIRATVGYSGYSQKFEFETGDETSDMAAEQGI-LVIATAVVGFTLLVILTL 567

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RESULT 5
US-09-922-138-2
; Sequence 2, Application US/09922138
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silius-Santiago, Immaculada
; TITLE OF INVENTION: 16658, 14223, AND 16002, NOVEL HUMAN
; FILE REFERENCE: 38155-20030.00
; CURRENT APPLICATION NUMBER: US/09/922,138
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/229,299

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; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-138-2

```

```

Query Match          48.7%; Score 1410; DB 5; Length 1130;
Best Local Similarity 48.0%; Pred. No. 1.5e-112;
Matches 259; Conservative 106; Mismatches 163; Indels 12; Gaps 7;

```

```

QY 9 LMDSTATAELGMVHPSPGMEVSGYDENMNTITRTYQCNVFESSONNMLTRKRRRG 68
D 131 LDDTTVLGELGKRTYPLNGMDATTEMDENRPIHTYQCNVMEPNONNMTRNWSRDA 190
QY 69 AHRHVEKRSVRCSSIPSPGCKETFNLYYEADFSATRTFPMNMPVVKYDTIA 128
D 191 AOKIYEMKFTLRDCNSIPWVLGCTKETFNLFYMESESHGKFRP----NOYTKIDTIA 246
QY 129 ADEFSQVDLGRVAKINTFVRSRSGFYLAFOYGGCMSLIAVRYFKCRPIIQ 188
D 247 ADESTQMDLGRILKNTREVGPIERKGFYLAFODIGACIALVSRYFYKCCPFYVR 306
QY 189 NGAIQETLSGAESTSLVAARGSCIANAEEDVPRIKLYCNGDEWLPIGRCKAKGFEA 248
D 307 NLAMPPTIRPVSSSLVEVRGSCVKSABERDTP-KLYCGADMDLVPILGRICSTGYEE 365
QY 249 VENGTVGCGSGTFRKANOGDEACTHCPINRRTSGATNCVCRNGYRADLPLDMPCT 308
D 366 IEGS--CHACRPFFYAFAGNTKSCPCPSHSLTYMEATSVCCCKEYFAAEKDPMSMACT 423
QY 309 TTPSAPQAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSGSGRACRCGDVVOYA 368
D 424 RPPSAPRVNVEFINETALLIEMSPSDTGKRDLYSVICKKCGLDTSQCECCGGGLRPI 483
QY 369 PROGLTEPRITYSDLAHQVTFEIOAVNGVTDQSPSPQ--FASVNTTNOAPSASVI 427
D 484 PRHTGLINNSVIVLDFVSHVNTFEIEMNGVSELS-FSPKPFRTIYVTTDDAPSLIGV 542
QY 428 MQVSRVDSITLSMSQPDOPNGVILDELOYEKEKELSE--YNATAIKSPNTVYGLKAG 485
D 543 VRKQWASQNSIALSMQAPAFNSGAILDYEIKIYKEKEHEGLTSSRSKAPSVITIGLPA 602
QY 486 AIYVFOVARTVAGYGRYSGKMYFQTMTEAEYQTSIOEKPLIIGSSAAGLVFLAVVVI 545
D 603 TKYVFHIRVIRATVGYSGYSQKFEFETGDETSDMAAEQGI-LVIATAVVGFTLLVILTL 661

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```

RESULT 6
US-09-971-708-3
; Sequence 3, Application US/09971708
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Human EphA6 Gene and Polypeptide
; FILE REFERENCE: OGT 16U 102 R1
; CURRENT APPLICATION NUMBER: US/09/971,708
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-971-708-3

```

```

Query Match          48.2%; Score 1395; DB 5; Length 1035;
Best Local Similarity 47.3%; Pred. No. 2.5e-111;
Matches 255; Conservative 105; Mismatches 169; Indels 10; Gaps 5;

```

OY	1	INDSTATATELGMMVHPPSGMEVEVSGYDENMANTIRIYOYCNFPESSONNMUTRKRRIIRRG	68
Db	36	LIDTITVIMGLKMKYTPPLNGMDAITEMDHNNRPIRHYYOYCNMEPNRNMWLTNNISDA	95
OY	69	AHHIHYEMKTSVDDCSISPSDGCKEFENLYYYEADFSAKTETPPNMENPWVAVDTA	128
Db	96	AORIIYEMKTKTLDDCNSIPWVLGTCKETENLIYIEEDBSHGKFKR---SQYIKIDFTA	151
OY	129	ADESFSDVLDGCHVMKINTEVRSFGVSRSGFYLAFODYGGCKSLIAVYVYFRKCPRIQ	188
Db	152	ADESFYQMDIGDRILKANTEIREVGPTEKRGFYLAFODIGACIALAVSVYFYKCCPFR	211
OY	189	NGAIPOETLSGABESTSVLAARGSCIANAEVVDPIKLYCNGOGEMLVPIGRCKCKAGFEA	248
Db	212	SLAFPPITPRIVSSSLVEVRGCVSKVAERDPP-KLYGCADDMLVPLGRCLCSGYEE	270
OY	249	VENGTVGRGCGSGCFKRNQGDCACTHCPINRSRTSEGATNCVCRNGYRRADDPLDMCT	308
Db	271	IEGS--CHACPGYTKAFAGNTKCSKCPPISSIFYEATSVCHCEKGCFRAEKPDPSPMACT	328
OY	309	TIPSAPOAVISSVNETSLMEWTPRPDSGGRDLVYIILKSCGSGGAGCATRGGDNVOYA	368
Db	329	RPPSAPFRVAVENINETAILEMSPSPSTGCKRDLTYIVICKKGCLDTQCEDCGGGIRFI	388
OY	369	PROGLTEPRYIISDLAHTOYFEIOAVNVTDOQSFSPQAFASVNTITNOAPSAYSIM	428
Db	389	PHHTLNNVAVLDFVSHVNTPEIEEMANGVSELSISPKRFATIVTTDHPADSLIGMM	448
OY	429	HOVSRTVDSITLSMSQDPDPNGVILDELOYEKEKELSE--YNATAISPTNTVYGLKAGA	466
Db	449	RKDMASNSLALSMQAPFNSGAILIDETAKYEEKHEHDLTYSRSPKASVYVGLMPAT	508
OY	487	IYFQVQRAITVAGYGRYSGKMYFOHMTAEAYOTSIOEKLPLITSSAAGLFLIAVVI	545
Db	509	TYFIHRTAFTAGYSGYSOKFEFEIETDETSKMAAQGI-LVIMATAAGGFTLLVILTL	566
RESULT 7			
PCT-US01-30539-4			
/ Sequence 4, Application PC/TUS0130539			
/ GENERAL INFORMATION:			
/ APPLICANT: PE CORPORATION (NY)			
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC			
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES			
/ TITLE OF INVENTION: THEREOF			
/ FILE REFERENCE: CL001156PCT			
/ CURRENT APPLICATION NUMBER: PCT/US01/30539			
/ CURRENT FILING DATE: 2001-03-06			
/ PRIOR APPLICATION NUMBER: 09/99,345			
/ PRIOR FILING DATE: 2001-03-06			
/ NUMBER OF SEQ ID NOS: 6			
/ SOFTWARE: FastSeq for Windows Version 4.0			
/ SEQ ID NO 4			
/ LENGTH: 265			
/ TYPE: PRT			
/ ORGANISM: Rattus norvegicus			
PCT-US01-30539-4			

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Db      133 KIDPIADESEFTOGDILGERKKKLTVEVREIPLSKRGFIYLAFOQVGCIALVSVKYYKK 192
QY      183 CPRTTONGAIFOEELLSGAESTSLVAARGSCIANA-EEVDVPFKITCYCNGDEMLYPISRCM 241
        | ||| :||:::||:|||| ||::||| ||::||| ||::||| ||::||| ||::||| ||::|||
Db      193 CWSIIENIAVPPDVDTGSEFSSTLVEVRKTCVSSAEFEAAENSPRMHCSAGEMLVIPIGKCI 252
QY      242 CKAGFEAVENGIVC 255;
        ||||: :|||
Db      253 CKAGYO-QKGDTG 264

RESULT      8
PCT-US01-30539-5
; Sequence 5, Application Pct./JUS0130539
; GENERAL INFORMATION:
; APPLICANT: PE CORPORATION (NY)
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001156PCT
; CURRENT APPLICATION NUMBER: PCT/US01/30539
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 09/799,345
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 265
; TYPE: prf
; ORGANISM: Mus musculus
PCT-US01-30539-5
```

	Query Match	27.1%	Score 784.5;	DB 1;	Length 265;	
	Best Local Similarity	56.7%;	Pred. No. 1,1e-59;			
	Matches 144;	Conservative	48;	Mismatches 55;	Indels 7;	Gaps 3;
Oy	3	AAVEETLMDSTTAETAGVMVHPSPSGMEVSQYDENMNTITTYOVCNVPESQNNMLRTK	62			
		: : : : :				
Dd	17	AAKEVLILDDSKAQGLETEIMSSPPSCMEHISGLDENTYPIRITYOCVOMENQNNMLRTIN	76			
Oy	63	FIRRRGAHRIVHEKTSVRDCSSIPESPSCKETNTIYYEADDFSAATKPENNMENPVY	122			
		: : : : : : : : : : : : : : : :				
Dd	77	WISGNQRIFVELKFTLRDCNSLPVELDTCKETENLYLEEDVD---TGRNRLENLYV	132			
Oy	123	KVDTLIAADESFQVLDGGRYMKTFNEFVSFGVSSGFIARFDODYGGMSLIAVAVEYRK	182			
		: : : : : : : : : : : : : : : : :				

```

Query Match      27.1%; Score 783.5; DB 1; Length 265;
Best Local Similarity 56.3%; Pred. No. 1.3e-59;
Matches 143; Conservative 49; Mismatches 55; Indels 7; Gaps 3;

QY      3 AAVEETLMDSTATAIEIGMVAHPSPSGMEVSGYGENMNTIFTYQVCVWFESSQNNMLRTK 62
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      17 AAEEVILLDKSKAQOETELIEWISSPSPGMEISLQDBNTPITFTYQVCYMEPNQNNMLRTN 76
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      63 FIRRGARHRYHEMKFVSVDSSIFSPGSGKETENLYYEAADPSATKTFPNMMENPMV 122
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      77 WISKGNQRIETFEIKTLTDCNSLPGVLGTCKETENLYYENDYD---TGRRNREINLYV 132
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      123 KVFPIADESFSGVDJGVRMKINTEFVSGVSSSGTYLAFOYGGCMSLIAYVFEYRK 182
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      133 KIDPIADESFQGGDJERMRKINTEFVRIGLPLSKGFLAQQDVGACTALVSKVYIKK 192
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      183 CPRIQNGAIFQETLSAESTSLVYARGSCINA--EVDVPYIKLYCNDGEMLVPIGRCM 241
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      193 CMTLVENLVAEPPTLVGSEFSSLVEYRGICVSAEEEAENSPRHMCSAEGEMLVPIGRCI 252
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      242 CKAGEAEEVENGTCV 255
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      253 CKAGYQ--QKGDTC 264
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      9
PCT-US01-30539-6
; Sequence 6, Application PC/TU0130539
; GENERAL INFORMATION:
; APPLICANT: PE CORPORATION (NY)
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001156PCT
; CURRENT APPLICATION NUMBER: PCT/US01/30539
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 09/799,345
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0

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SEQ ID NO 6
LENGTH: 265
TYPE: PRT
ORGANISM: Mus musculus
PCT-US01-30539-6

Query Match 27.1%; Score 783.5; DB 1; Length 265;
Best Local Similarity 56.3%; Pred. No. 1.3e-59;
Matches 143; Conservative 49; Mismatches 55; Indels 7; Gaps 3;

QY 3 AAVETLMDSTATAELGMMVHPSPSGMEVSGYDENMTTIRTYOVANVFESSONNMILRTK 62
DB 17 AAKVILLDSKASQAELEWISSPPSGMEISGIDENYPIRTYOVCOVMEQNMMILRTN 76
QY 63 FIRRGAHRIHEVEMKFSVRCSSIPSVGSKETENLYYEADSDSKTFFPMNEMPMV 122
DB 77 WISGNMORFVELKFTLRBCNSLPGLGTCKETFNLYETDID---TGRNIREMLYV 132
QY 123 KVDITADESFQVDLGRVWKINTEVRSFQVRSRGFYLAFOVGGCMLIAVRFYRK 182
DB 133 KIDITADESFQDGLGERMKMLNTEVREIGPLSKGFYLAFOVGACIALVSVKYRK 192
QY 183 CPRTIONGALFOETLSAESTSLVAAGSCIANA-EVDVPIKLYCGDDEMLVPIGRMC 241
DB 193 CMTIVENLAVFPDVTGSEFSLVEVRGTCVSSAEFEAENSPPRMHCSAEDEMLVPIGRCI 252
QY 242 CKAGFEAVENGTVIC 255
DB 253 CKAGYQ--QKGDTC 264

RESULT 10
PCT-US01-30539-2
Sequence 2, Application PC/TUS0130539
GENERAL INFORMATION:
APPLICANT: PE CORPORATION (NY)
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001156PCT
CURRENT APPLICATION NUMBER: PCT/US01/30539
CURRENT FILING DATE: 2001-03-06
PRIOR FILING DATE: 09/799,345
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 295
TYPE: PRT
ORGANISM: Human
PCT-US01-30539-2

Query Match 23.7%; Score 686; DB 1; Length 295;
Best Local Similarity 51.4%; Pred. No. 3.5e-51;
Matches 131; Conservative 46; Mismatches 74; Indels 4; Gaps 3;

QY 4 AAVETLMDSTATAELGMMVHPSPSGMEVSGYDENMTTIRTYOVANVFESSONNMILRTK 63
DB 33 AAEVILLDSKASQAELEWISSPPSGMEISGIDENYPIRTYOVANVFESSONNMILRTN 92
QY 64 FIRRGAHRIHEVEMKFSVRCSSIPSVGSKETENLYYEADSDSKTFFPMNEMPMV 123
DB 93 ISRGRCGRIFVELQFTLRCCSSIPGAGCTKETFNLYETEDLQ-RGRPRIGSGRPK 151
QY 124 VDTIADESFQVDLGRVWKINTEVRSFQVRSRGFYLAFOVGGCMLIAVRFYRK 183
DB 152 IDTIADESFQDGLGERMKMLNTEVREIGPLSKRGFHLAFOVGACIALVSVKYRK 211
QY 184 PRIONGALFOETLSAESTSLVAAGSCIANA-EVDVPIKLYCGDDEMLVPIGRMC 242
DB 212 RATVKGALFPAATASAFSTLVEVAGTCVAHSEGGSPRMRHCGADGEMLVIPVGRSC 271

QY 243 KAGFEAVENGTVIC 257
DB 272 SAGFO--ERGDICG 284

RESULT 11
US-09-922-138-10
Sequence 10, Application US/09922138
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: Kinases, Immaculada
TITLE OF INVENTION: KINASES AND USES THEREFOR
FILE REFERENCE: 38155-20030.00
CURRENT APPLICATION NUMBER: US/09/922,138
CURRENT FILING DATE: 2001-11-28
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 178
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid sequence
US-09-922-138-10

Query Match 23.4%; Score 678; DB 5; Length 178;
Best Local Similarity 68.7%; Pred. No. 8.6e-51;
Matches 123; Conservative 26; Mismatches 28; Indels 2; Gaps 2;

QY 6 EETLMDSTATAELGMMVHP-PSGMEVSGYDENMTTIRTYOVANVFESSONNMILRTK 64
DB 1 EYLLDTKTATGELGMLTYVPVPSGMEVSGLDENNRPIRTYOVANVFESSONNMILRTN 60
QY 65 RRGGAHRIHEVEMKFSVRCSSIPSVGSKETENLYYEADSDSKTFFPMNEMPMV 124
DB 61 ERGAHRIHEVEMKFSVRCSSIPSVGSKETENLYYEADSDSKTFFPMNEMPMV 124
QY 125 DITIADESFQVDLGRVWKINTEVRSFQVRSRGFYLAFOVGGCMLIAVRFYRK 183
DB 120 DITIADESFQVDLGRVWKINTEVRSFQVRSRGFYLAFOVGGCMLIAVRFYRK 178

RESULT 12
US-09-922-138-12
Sequence 12, Application US/09922138
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: Kinases, Immaculada
TITLE OF INVENTION: KINASES AND USES THEREFOR
FILE REFERENCE: 38155-20030.00
CURRENT APPLICATION NUMBER: US/09/922,138
CURRENT FILING DATE: 2001-11-28
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 180
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid sequence
US-09-922-138-12

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 1, 2002, 09:54:55 ; Search time 26.14 Seconds
(without alignments)
1550.933 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 5116

Sequence: 1 LLAABETLMDSTATAELG.....ILNSTQVMAQMNQIQSVEV 970

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 202503 seqs, 41795235 residues

Total number of hits satisfying chosen parameters: 202503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_AA_New:

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pap.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pap.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pap.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pap.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pap.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pap.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3899.5	76.2	984	7	US-60-341-631-3
2	3014	58.9	1037	7	US-60-339-995-3
3	2837	55.5	1036	5	US-09-971-708-2
4	2837	55.5	1035	5	US-09-922-138-2
5	2811	54.9	1035	5	US-09-971-708-3
6	2161.5	42.2	942	6	US-10-004-542-2
7	1793	35.0	406	5	US-09-760-446A-1452
8	1150	22.5	270	5	US-09-760-446A-1496
9	1103.5	21.6	277	5	US-09-760-446A-1538
10	822	16.1	189	5	US-09-760-446A-2141
11	784.5	15.3	265	1	PCT-US01-30539-4
12	783.5	15.3	265	1	PCT-US01-30539-5
13	783.5	15.3	265	1	PCT-US01-30539-6
14	771	15.1	308	6	US-10-004-542-4
15	771	15.1	334	5	US-09-971-708-5
16	686	13.4	295	1	PCT-US01-30539-2
17	684	13.4	190	5	US-09-760-446A-1492
18	678	13.3	178	5	US-09-922-138-10
19	672	13.1	222	5	US-09-760-446A-2225
20	670	13.1	204	5	US-09-760-446A-2137
21	666.5	13.0	180	5	US-09-922-138-12
22	639.5	12.5	206	5	US-09-760-446A-1652
23	597	11.7	1382	5	US-09-971-873-7
24	595	11.6	351	5	US-09-760-446A-1339
25	595	11.6	541	5	US-09-864-291-20
26	594	11.6	509	5	US-09-971-873-8

27	591	11.6	376	5	US-09-760-446A-2013	Sequence 2013, Ap
28	586	11.5	256	5	US-09-967-854-4	Sequence 4, Appl1
29	586	11.5	256	5	US-09-840-704-4	Sequence 4, Appl1
30	576.5	11.3	1138	6	US-10-021-660-101	Sequence 101, Appl
31	574	11.2	271	5	US-09-971-873-41	Sequence 41, Appl
32	562.5	11.0	1256	6	US-09-632-507A-2	Sequence 2, Appl1
33	554	10.8	280	6	US-10-003-690-8	Sequence 8, Appl1
34	551	10.8	823	5	US-09-886-319A-63	Sequence 63, Appl
35	549.5	10.7	1256	5	US-09-632-507A-14	Sequence 14, Appl
36	547	10.7	822	5	US-09-886-319A-64	Sequence 64, Appl
37	539.5	10.5	1124	6	US-10-021-660-112	Sequence 112, Appl
38	539	10.5	1255	5	US-09-806-703A-4	Sequence 4, Appl1
39	538.5	10.5	937	5	US-09-974-298-129	Sequence 129, Appl
40	538	10.5	1255	5	US-09-632-507A-1	Sequence 1, Appl1
41	537	10.5	619	5	US-09-971-873-9	Sequence 9, Appl1
42	531.5	10.4	260	6	US-10-029-386-33374	Sequence 33374, A
43	530	10.4	885	1	PCT-US01-24104A-52	Sequence 52, Appl
44	522	10.2	822	5	US-09-966-147-2	Sequence 2, Appl1
45	520.5	10.2	1210	5	US-09-725-433-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-60-341-631-3
; Sequence 3, Application US/60341631
; GENERAL INFORMATION:
; APPLICANT: Spaltmann, Frank
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; FILE REFERENCE: MPI2001-293P1(M)
; CURRENT APPLICATION NUMBER: US/60/341, 631
; CURRENT FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Homo Sapien
US-60-341-631-3

Query Match 76.2%; Score 3899.5; DB 7; Length 984;
Best Local Similarity 73.8%; Pred. No. 3.4e-274;
Matches 712; Conservative 130; Mismatches 120; Indels 3; Gaps 2;

Qy	2	LAABETLMDSTATAELGWMVHPSPSGWEEVSGYDENNTTIRTYQVCNVFPSSONMLRT	61
Db	15	VAMETLMDTATAEGLGTANPASGWEVSGYDENLNTIRTYQVCNVFPNNMLLT	74
Qy	62	KPIRRGAHRIHVEMKFSVRDCSSIPSPGSKETFNLYYEADFDSATKTFPNNMNPW	121
Db	75	TFINRRGAHRIYEMRTFVRDCSSILPNVPGSKETFNLYYETSVATKSAFWSAPY	134
Qy	122	VKVDIAADESFSQVLDGGRVKNKINTEVRSGPVSRSGFYLAFOYGCMSLIAVRVYR	181
Db	135	LKVDPTIAADESFSQVDFGRLMKVNTVEVSFGPLTRNGFYLAFOYGCMSLLSVRVEK	194
Qy	182	KCPRIQNGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGLWLPICRM	241
Db	195	KCPSLVQNFVFPETMTGAESTSLVARGCIPNAEEVDVPIKLYCNGDGLWLPICRGT	254
Qy	242	CKAGFEAVENTVCGPCSGCTFKANQGDCACTHCPINSTRTTSECATNCVCRNGYRADLD	301
Db	255	CKPGYEP-ENSVACKACPACTFKASQEAEGSCHSPNSRSPAEASPICTCTGYRADFD	313
Qy	302	PLDMPCITISAPQAVISSVNETSLMLEWTPDRDSGGREDLVNIIKSCGSGRGATRC	361
Db	314	PPEACTSVSPGPRNVISVNETSIILEWHPHPTGTGDDVTYNIICKRADRRSCRC	373
Qy	362	GDNVQYAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPFPQFASVNTTNOAA	421

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RESULT      2
US-60-339-995-3
; Sequence 3, Application US/60339995
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: Methods and Compositions to Treat
; TITLE OF INVENTION: Cardiovascular Disease Using 1419, 58765 and 2210
; FILE REFERENCE: MPI2001-291P1(M)
; CURRENT APPLICATION NUMBER: US/60/339,995
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-60-339-995-3

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RESULT 3
US-09-971-708-2
; Sequence 2, Application US/09971708
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Human EpiA6 Gene and Polypeptide
; FILE REFERENCE: OCT 16U 102 R1
; CURRENT APPLICATION NUMBER: US/09/971,708
; CURRENT FILING DATE: 2001-10-09

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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo sapien
us-09-971-708-2

Query Match 55.5%; Score 2837; DB 5; Length 1036;
Best Local Similarity 53.6%; Pred. No. 3.4e-197;
Matches 539; Conservative 167; Mismatches 240; Indels 60; Gaps 13;

QY 9 LMDSTTATAEALGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSONNWLRTKFIIRRG 68
Db 37 LDDTTTVLGLGWKTYPLNGWDAITEMDEHNRPITHYQVCNVFESSONNWLRTNWSIDA 96
QY 69 ARIHIVEMKESVRDCSSIPSPGCKETFNLYYEADPDSATKTFPNMNPWKVDTIA 128
Db 97 AOKIYVEMKFTLRDCNSIPWLGTCETFNLFYMESDESHGKFKP-----NOYTKIDTIA 152
QY 129 ADESFQVDLGLGRVNMKINTEVRSGFVSRSFYLAFOYDYGCMSLIAVRVYKCPRII 188
Db 153 ADESFQMDLGRILKLTREVEGPIERKGYLAFOYDYGCMSLIAVRVYKCPRII 188
QY 189 NGAIQFETLSGAESTSLVAARGSCIANAEVDVPILKLYCNGDGEWLVPICRCMKAGFEA 248
Db 213 NLAMPDPPIPRVDSLSVEVSGVSKAEERDTP-KLYCGADGDMVPLGRCICSTGYEE 271
QY 249 VENGTVRCGSPGTFKANOQDEACTHCPINRSTTSEGATNCVCRNGYRADLDPDMPT 308
Db 272 IEGS--CHACRPGFYKAFAGNTKCKPPHSLTYMEATSVQCCEKGYFRAEKDPSPMACT 329
QY 309 TIPSAPQAVISSVNETSLMLEWTPPRSGGREDLVYNIICKSCSGRGACTRCGDNVQYA 368
Db 330 RPPSAPRNVFNINETAILEWSPSDTGGKDLTYSVICKKGLDTSQCDGCGGLRFI 389
QY 369 PRQLGLTEPRIYISDLLAHTQYTFEIOAVNGVTDQSPSPQ-FASVNIITNOAPSASVI 427
Db 390 PRHTGLINNSVIVLDFVSHVNYTFEIAMNGVSELS-FSPKPTAITVTTDQAPSLIGV 448
QY 428 MHQVSRVDSITLWSQDPDQNGVILYQYKEKELSE--YNATAIKSPNTVTGLKAG 485
Db 449 VRKDWASONSIALSWQAPAFSNGAILDYEIKYKEHEQULTYSSSTRSKAPSVIITGLKPA 508
QY 486 AIYVQVQVARTVAGYGRYCKMYFQTMTEAEYQTSIQEKLPLIIGSSAAGLVFLIAVVI 545
Db 509 TKYVFHVRVATATGYSGYSQKFEFETGDETSDMAEQQGLVLTATAVGGFTLLVILTLF 568
QY 546 AIVCNR-RGFERADSEYTDKIQ-HYTSGHIT-PGMKIYIDPFTYEDPNEAVREFAKEIDI 602
Db 569 FLITGRQWYIKAMKSEKKRRNHLNGHLRFPFGIKTYIDPDYEDPSLAVHEFAKEIDP 628
QY 603 SCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYKEKORRDLFSLASINGQFD 662
Db 629 SRIRIERVIGAGEFGEVCSGLATPKGREIPVAIKTLKGHMDRQRDLFSLASINGQFD 688
QY 663 HPNVHLEGVVTWT-----PVM 680
Db 689 HPNIILEGVYKRSFPAIGVEAFPCFLRAGFLNSIQAPHPVPGGSLPPIPRIPAGRPVM 748
QY 681 IITFEMENGLSDFLRQNDQOFTVIQVGLMRLGIAAGMYLADMYVVRHDLAARNILVNS 740
Db 749 IIVVEYENGLSDFLRKHGHQHTFVIQVGLMRLGIAAGMYLADMYVVRHDLAARNILVNS 808
QY 741 NLVCKVSDGLSFLRLEDDTSDPTTYSALGKFPPIRWTAPEAIQYKFTSASDWSYGLVM 800
Db 809 NLVCKVSDGLSFLRLEDD-PEAAYTTT-GGKIPRIWTAPEAIYKFTSASDWSYGLVM 866
QY 801 WEVMSYGERPYWDWTDVINAIEDQYRLPPMDPCPSALHQLMDCWQRNRHPRKFOI 860
Db 867 WEVMSYGERPYWMSNQDVIILSEEGYRLPAPMGCPASLHQLMDCWQRNRHPRKFOI 926

QY 861 VNTLDKMRNPNSLKAMAPLSSGINLPDLRTIPDYTSTNTVDLEAIKMGYKESFAN 920
Db 927 VSPDLKLRNPSSALHTL--VEDILVMPESPGEVPEPLFVTVGDWLDLSIKMGYKNEVA 984
QY 921 AGTTSFSDVVSQMMEDILRVGTVLAGHQKILNSIQVMRAQMNQIQ 966
Db 985 AGFTTFDLISMSIDDIRRIGVILIGHQRIRIVSSIQTLRLHMHQI 1030

RESULT 4
US-09-922-138-2
; Sequence 2, Application US/09922138
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 16658, 14223 AND 16002, NOVEL HUMAN
; TITLE OF INVENTION: KINASES AND USES THEREFOR
; FILE REFERENCE: 38155-20030.00
; CURRENT APPLICATION NUMBER: US/09/922,138
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/229,299
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-138-2

Query Match 55.5%; Score 2837; DB 5; Length 1130;
Best Local Similarity 53.6%; Pred. No. 3.9e-197;
Matches 539; Conservative 167; Mismatches 240; Indels 60; Gaps 13;

QY 9 LMDSTTATAEALGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSONNWLRTKFIIRRG 68
Db 131 LDDTTTVLGLGWKTYPLNGWDAITEMDEHNRPITHYQVCNVFESSONNWLRTNWSIDA 190
QY 69 ARIHIVEMKESVRDCSSIPSPGCKETFNLYYEADPDSATKTFPNMNPWKVDTIA 128
Db 191 AOKIYVEMKFTLRDCNSIPWLGTCETFNLFYMESDESHGKFKP-----NOYTKIDTIA 246
QY 129 ADESFQVDLGLGRVNMKINTEVRSGFVSRSFYLAFOYDYGCMSLIAVRVYKCPRII 188
Db 247 ADESFQMDLGRILKLTREVEGPIERKGYLAFOYDYGCMSLIAVRVYKCPRII 306
QY 189 NGAIQFETLSGAESTSLVAARGSCIANAEVDVPILKLYCNGDGEWLVPICRCMKAGFEA 248
Db 307 NLAMPDPPIPRVDSLSVEVSGVSKAEERDTP-KLYCGADGDMVPLGRCICSTGYEE 365
QY 249 VENGTVRCGSPGTFKANOQDEACTHCPINRSTTSEGATNCVCRNGYRADLDPDMPT 308
Db 366 IEGS--CHACRPGFYKAFAGNTKCKPPHSLTYMEATSVQCCEKGYFRAEKDPSPMACT 423
QY 309 TIPSAPQAVISSVNETSLMLEWTPPRSGGREDLVYNIICKSCSGRGACTRCGDNVQYA 368
Db 424 RPPSAPRNVFNINETAILEWSPSDTGGKDLTYSVICKKGLDTSQCDGCGGLRFI 483
QY 369 PRQLGLTEPRIYISDLLAHTQYTFEIOAVNGVTDQSPSPQ-FASVNIITNOAPSASVI 427
Db 484 PRHTGLINNSVIVLDFVSHVNYTFEIAMNGVSELS-FSPKPTAITVTTDQAPSLIGV 542
QY 428 MHQVSRVDSITLWSQDPDQNGVILYQYKEKELSE--YNATAIKSPNTVTGLKAG 485
Db 543 VRKDWASONSIALSWQAPAFSNGAILDYEIKYKEHEQULTYSSSTRSKAPSVIITGLKPA 602
QY 486 AIYVQVQVARTVAGYGRYCKMYFQTMTEAEYQTSIQEKLPLIIGSSAAGLVFLIAVVI 545
Db 603 TKYVFHVRVATATGYSGYSQKFEFETGDETSDMAEQQGLVLTATAVGGFTLLVILTLF 662
QY 546 AIVCNR-RGFERADSEYTDKIQ-HYTSGHIT-PGMKIYIDPFTYEDPNEAVREFAKEIDI 602

[illegible]

	QY	309	TIPSAOAVISSVNETSLMLEWITPPRSDSGREDLVYNIICKSCGSGRGACTRCGDNVOYA	368
	Db	329	RPSAPRNVAFINETALILEWSPPDGTGRKDLITYSVICKKGLDTTQCDSGGGLRFI	388
	QY	369	PROLGLTEPRIYSIDLLAHTQYTFFELQAVNGVTDOOSPSPOFASVNITNQAAPSIVM	428
	Db	389	PRHTGLINNVSVVLFDFVSHVNTFIEAWNGVSELSISPKPFTAITVTTDDAFSLICMM	448
	QY	429	HQVSRVTDTSILTSWSPODOPONGVILDYELQYYEKELSE--YNATAIKSPTNVTVGLKAGA	486
	Db	449	RKWASONSLALSQWAPAFNSGAILLDYETKYEKEHEQLTYSSRSKAPSVITVTLGPAT	508
	QY	487	IYFOVRARTVAGYGRYSKMTQFMWTAEYQTSIOEKLPLIIIGSSAAGLFLIAVVVIA	546
	Db	509	TVIFHVRVATGYCYGSKOFFETGDETSMAAQGOILVIATAAVGFTLLVLTUUFF	568
	QY	547	IYCNR-RGERADSEYTDKLO-HYTSGHIT-PGMKIYIDPFYEDNEPAVREFAKEIDIS	603
	Db	569	LITGRQWYIKAMKSEERKTHLQNGHLRFPGIKTYIDPDYEDPSLAVHFAKEIDPS	628
	QY	604	CVKIEQVIGAGEFGVCVCSGHLKLPKKRETFVAILKTKSGYTEKQRDELSEASIMQOFDH	663
	Db	629	RIRIERVIGAGEFGVCSGRLKTPGKRREIPVAIKTLKGHMDQRDRDFUREASIMQOFDH	688
	QY	664	PNVILHLEGVVVKST-----PVMV	681
	Db	689	PNRIURLEGVVVKTSFFPAIGVEPCSFRLAGFLNGIQAPHVPVTAGSSLPPRIAPGRPVMV	748
	QY	682	ITEBFMENGLSDSLFRNQDGOFTVLIQVLMRLGIAAGMKYLADMYVHRDLAARNILVSN	741
	Db	749	VVEYMENGLSDSLFRKHGDHFTVLIQVLGMLRTIASMGKYLSDMGYVHRDLAARNILVSN	808
	QY	742	LVCVKSDFGLSRLEDDTSDPTVTSALGGKFPIRWTAPEAIQYRKFTSASDVMSXGIVMW	801
	Db	809	LVCVKSDFGLSRVLEDD-PPAAVTTT-GGKIPRWTAPEALAYRKFSASDAWSXGIVMW	866
	QY	802	EVMXYGERPYWMNTQNQVINAIQEYDLRPPMPDCPSALHOLMCDQWKORNHRRPKFQIV	861
	Db	867	EVMXYGERPYWEWSNQDIVLSIBEGYRLPAMPGPCPSLQOLMLHCWKORNHRRPKFTDIV	926
	QY	862	NYLDKMITNPNSLKAMAPLSSGNLPLLDRTIPDYTSFNVDSEWLAKMGQYKESFANA	921
	Db	927	SFLDKLIRNPSALHTL--VEDILVMPSPGDVEYPFLFVTVGDWLDISKMGQYKSNFMAA	984
	QY	922	GFTSFDVYVSQMMEIDLVRGVTLAGHQKITLNSIQVMNAOMNOIQ	966
	Db	985	CFTTFOTITSMISIDIRIGVILIGHORRIVSSIQITLRLLHHMIQ	1025

```

RESULT      6
US-10-004-542-2
; Sequence 2, Application US/10004542
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Walke, D. Wade
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinase and Polynucleotides
; FILE REFERENCE: Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/004,542
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/243,893
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 942
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-004-542-2

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Query Match          42.2%; Score 2161.5; DB 6; Length 942;
Best Local Similarity 51.8%; Pred. No. 2.6e-148;
Matches 416; Conservative 133; Mismatches 200; Indels 57; Gaps 11;

Qy 9 LMDSTTAAELGMVHPSPGWEVSGVDENMNTIRYQVCNVFESSONNKLRTKFFRRRG 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 LLDTTTTLGELGKWTPLNGMDAITDEHNRPITHTYQVCNVFESSONNKLRTNISRDA 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 69 ARIHVEKESVRDCSIPSPGSKETNLYYYEADFSATKTFENMMENPWVVDITA 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 AKLIYDMKFTLDCNSIPVLTGCTKTENLFYMESDESHGKFKP---NQTIDITA 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 129 ADEFSQVDLGGVMTINTEVRSGFVPSRSGFLAFQDYGGCMLIAVRFYRKCPRIIQ 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 ADESEFQMDLGRILALNTEIREVGPIERKGYLAFQDYGACIALVSVRFYKCPFTVR 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 189 NGAIFOETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPIGRMCCKAGFEA 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 307 NLAMFFDTIPRVDSLSLVEARGSCVKSABERDTP-KLYCGADGDLVPLGRICSTGIEE 365
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 249 VENGTVCRGCPSTFKANOGDEACTHCPINSTTSEGATNCVCRNGYYRADLPDMPCT 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 366 IEGS--CHACRGFYKAFAGNTKCKPSPHSUTYMEATSVCCCKGYPRAEKDPPSMACT 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 309 TIPSAPQAVISSNETSLMLEWTPPRDGGREDLVYNIICKSGRGACRCGDNVQYA 368
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 RPPSAPRVVFNINETALILEWSPSDTGGKRLTYSYICKKGLDTSQCDCCGGGLRFI 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 369 PROLGITPRIYISDLAHTQYTFBIQAVNGVTDQSPSPQ-FASVNITTNQAAAPSASI 427
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 484 PHTGLINNSVILDFVSHVNTYEIAHNGVSELS-FSPKPTAITVTTDQDAPSLIGV 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 428 MHQVSRVDSITLSWSQDPQNGVTLDELOYEYKELSE--YNATAIKSTNTVTGLKAG 485
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 VRKDWASQNSIALSQAFAFNSGAILDYEIYKEHEOLTYSTRSKAPSVIITGLKPA 602
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 486 ATYVPOVARTVAGRYGSKMYQOTWTEABYQTSIQEKLPLIITGSAAGLVFLIAVVI 545
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 TKYVPHIRVTRATGYSGYSEKFEETDETSDMAAEQQILVIATAVGGFTLLVITLF 662
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 546 AIVCNR-RGFERADSEYTKLQ-HVTSGHIT-PCMKTYIDPFYEDPNEAVREFAKEIDI 602
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 FLITGRQWYIKAKKSEKRNHLQNGHLPFOIKTYIDPDYEDPNSLAVHEFAKEIDP 722
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 603 SCVIEQVIGAGEGVCVSHGLKPGKREIFVAIKLKGTYTEKQRDRFLSEASIMGQFD 662
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 SRIRIERVIGAGEGVCVSGRLKTPGKREIPVAIKLKGCHMDRQRDRFLSEASIMGQFD 782
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 663 HPNVHLEGVVTKST-----PVM 680
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 783 HPNIIRLEGVVTKSRFPAIGVEAFCSFRLAGFLNSIQAPHPVPGGSLPPRIPAGRPVM 842
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 581 IITFEMNGSLDSFLRQNDQQTIVLQVGLRGIAAGMYLADMNVVRDLAARNILVNS 740
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 843 IVVEYMENGLDSFLRKRGHFTVQLVGNLRCIASGMKYLSDMGVYVHDLAARNILVNS 902
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 741 NLVCKVSDGLSFLRLEDTSDDPYTS 766
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 903 NLVCKVSDGLSFLRLEDD-PEAAIYT 927
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-760-446A-1452
; Sequence 1452, Application US/09760446A
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT268
; CURRENT APPLICATION NUMBER: US/09760.446A
; CURRENT FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: 60/179,065

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; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
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; PRIOR APPLICATION NUMBER: 60/225,758
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; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
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; PRIOR APPLICATION NUMBER: 60/218,290
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; PRIOR APPLICATION NUMBER: 60/226,868
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; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
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; PRIOR FILING DATE: 2000-07-26
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; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01

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Prior Filing Date:	2000-11-17
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Prior Filing Date:	2000-11-17
Prior Application Number:	60/249,297
Prior Filing Date:	2000-11-17
Prior Application Number:	60/232,400
Prior Filing Date:	2000-09-14
Prior Application Number:	60/231,242
Prior Filing Date:	2000-09-08
Prior Application Number:	60/232,081
Prior Filing Date:	2000-09-08
Prior Application Number:	60/232,080
Prior Filing Date:	2000-09-08
Prior Application Number:	60/231,414
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Prior Application Number:	60/231,244
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Prior Filing Date:	2000-09-14
Prior Application Number:	60/233,063
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Prior Filing Date:	2000-09-14
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Prior Filing Date:	2000-09-14
Prior Application Number:	60/232,401
Prior Filing Date:	2000-09-14
Prior Application Number:	60/241,808
Prior Filing Date:	2000-10-20
Prior Application Number:	60/241,826
Prior Filing Date:	2000-10-20
Prior Application Number:	60/241,786
Prior Filing Date:	2000-10-20
Prior Application Number:	60/241,221
Prior Filing Date:	2000-10-20
Prior Application Number:	60/246,475
Prior Filing Date:	2000-11-08
Prior Application Number:	60/231,243
Prior Filing Date:	2000-09-08
Prior Application Number:	60/233,065
Prior Filing Date:	2000-09-14
Prior Application Number:	60/232,398

Query Match
Best Local Similarity
Matches 33%; Conservative 32; Mismatches 37; Indels 4; Gaps

35.0%; Score 1793; DB 5; Length 406;
82.2%; Pred. No. 4e-122;

Qy	561	YTDKLQHYTSGHITPGMKIYIDFTVEDNEAVREFAKEIDISCVKIEOVICAGFEGVC	620
Db	1	YTXKLQY---IAPGMKVYIDFTVEDNEAVREFAKEIDISCVKIEEIVICAGFEGVC	56
Qy	621	SCHLKLPGKREIFVAIKTLASGYTEKORRDFLSEASIMGOFHPNVIHLGVVTKSTPYM	680
Db	57	RGRLLKPQGRREVFAIKTLKVGTERORRDLSEASIMGOFDHPNIIRLEGVVTKSRPYM	116
Qy	681	LITEFMENGLDSFLRNQDGFTYQLVGLMLRGIAAGMKYLADMNYYVHRDLAARNILVNS	740
Db	117	ILTFEMENCALDSFLRLNDGFTYQLVGLMLRGIAAGMKYLSMMNVVHRDLAARNILVNS	176
Qy	741	NLVCKVSDFGLSRELEDDTSPTYTSALGKFPIRTWTAPEAIORYKFTSASDWWSYGVM	800
Db	177	NLVCKVSDFGLSRELEDDSPDPTYSLGKGIPRIWTAPAETAIARYKFTSASDWWSYGVM	236
Qy	801	WEVWSYGERPYNMTNODVINAEIQDYRLPPMDPCPSALHOLMLDCWKQRNHRPKFGOI	860
Db	237	WEVWSYGERPYNMGSNQDVINAVEQDYRLPPMDCPALTACXMLDCWVRDNLRPKFSOI	296
Qy	861	VNTLDKMIRNPNSUKAMAPLSGINPLDLLDTFIIDYTFSFWTVDBWLEAIKMGOKESFAN	920

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;; PRIOR APPLICATION NUMBER: 60/249,218
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;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/231,243
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,065
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,398

Query Match 22.5%; Score 1150; DB 5; Length 270;
Best Local Similarity 82.4%; Pred. No. 8.5e-76;
Matches 216; Conservative 24; Mismatches 20; Indels 2; Gaps 2;
QY 588 DPNEAVREFAKEIDISCVKIEQVIGAGEGVCVSHLPLPKRRELFVAIKTLKSGYTEKQ 647
Db 1 DPQAVHEFAKEIAESCITIERVIGAGEGVCVSHLPLPKRRELFVAIKTLKSGYTEKQ 60
QY 648 RRDFLSEASIMGQFDHPNIIHLEGVVTKSPYMIITEFMENGSLDSFLRQNDGQFTVIQL 707

Db 61 RRDFLSEASIMGQFDHPNIIHLEGVVTKSPYMIITEFMENGSLDSFLRQNDGQFTVIQL 120
QY 708 VGMRLGIAAGMKYLAADNMYVRDLAARNILVNSNLVCKVSDFLGSLRFLSDTSDPTTSA 767
Db 121 VGMRLGISAAGMKYLSIDMGYVHRDLAARNILVNSNLVCKVSDFLGSLRFLSDTSDPTTSA 179
QY 768 LGKFPFIRWTAPEAIOYRKFTSASDVMSYGIYVMEVMSYGERPYWDMTNDVINAIEODY 827
Db 180 -GGKIPINWTAPEAIAERKFTSASDVMSYGIYVMEVMSYGERPYWDMTNDVINAIEODY 238
QY 828 RLPPPMDCPSALHMLDCWOK 849
Db 239 RLPPPMDCPSALHMLDCWOK 260
RESULT 9
US-09-760-446A-1538
; Sequence 1538, Application US/09760446A
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT268
; CURRENT APPLICATION NUMBER: US/09760,446A
; PRIOR FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
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; PRIOR FILING DATE: 2000-07-26
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; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
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72	PRIOR APPLICATION NUMBER: 60/232,398

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;; PRIOR APPLICATION NUMBER: 60/232,398

Query Match 16.1%; Score 822; DB 5; Length 189;
Best Local Similarity 79.6%; Pred. No. 3e-52;
Matches 152; Conservative 21; Mismatches 16; Indels 2; Gaps 2;

QY 682 IREFMENGSLDSEFLRQNDGQFTVQLVGLMGLGIAAGKYLADNMYVHRDLAARNILVNSN 741
Db 1 VTEMENGSLDTFLKKNDSQFTVQLVGLMGLGIAAGKYLADNMYVHRDLAARNILVNSN 60
QY 742 LVCKVSDFGSLRLEDDTSDPTYSALGCKFPIRTWTAPEAIOYRKETSASDVWSYGIYMW 801
Db 61 LVCKVSDFGSLRVLEDD-PEAYTTR-GGKIPRTWTAPEAIAFRKFTSASDVWSYGIYMW 118
QY 802 EVMSYGERPYWMTNODVINAIEDQYRLPPMDPCPSALHQLMDCWQKDRNHRPFQIV 861
Db 119 EVYSYGERPYWMTNODVIAKAVEGYRLPSMDPCPAALYQLMDCWQKERNRPFDEIV 178
QY 862 NTLDKMIRNPN 872
Db 179 NMLDKLIRNPS 189

RESULT 11

PCT-US01-30539-4
; Sequence 4, Application PC/TUS0130539
; GENERAL INFORMATION:
; APPLICANT: PE CORPORATION (NY)
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01156PCT
; CURRENT APPLICATION NUMBER: PCT/US01/30539
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 09/799,345
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Rattus norvegicus
PCT-US01-30539-4

Query Match 15.3%; Score 784.5; DB 1; Length 265;
Best Local Similarity 56.7%; Pred. No. 2.5e-49;
Matches 144; Conservative 48; Mismatches 55; Indels 7; Gaps 3;
QY 3 AAVEETLMDSTATAELGWMVHPSPSGWEEVSGYDENNMNTIRTYQVCNVPSSONNLRTK 62
Db 17 AKEVLLDLSKAQOTELEWISSPPSGWEEISGLDENYTPRTYQVCNVPSSONNLRTN 76
QY 63 FIRRGARHRTVENKFSVRDCCSSIPSPVSGCKETFNYEADFATKTFPNMNPW 122
Db 77 WISGNAQRIFFVELKFTLRDCNSLPGVLGTCKETFNYEADFATKTFPNMNPW 132
QY 123 KVDITIAADESFQVDLGGVYMKINTVRSRGSFYLAEODYGCGLSLAVRVYRK 182
Db 133 KIDTIADESFQVDLGGVYMKINTVRSRGSFYLAEODYGCGLSLAVRVYRK 192
QY 183 CPRIQNGAIFQETLSGAESTSLVAARGSCIANA-EVDVPIKLYCNGDGEWLVPICRGM 241

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; ORGANISM: Mus musculus
PCT-US01-30539-6

Query Match 15.3%; Score 783.5; DB 1; Length 265;
Best Local Similarity 56.3%; Pred. No. 3e-49;
Matches 143; Conservative 49; Mismatches 55; Indels 7; Gaps

QY 3 AAVEETIMDSYTAELGHWVHPSPSGWEVSGYDENMNTIRTQVCNVFSSQNWLRTK 62
Db 17 AAKEVILLDSKAQQTLEWISSPPSGWEISGLDENYPTIFTYQVCQVMEPNQNLRTN 76
QY 63 FIRRGARHRIHVEMKFSVRDCSSIPSPCKSEKTFNLVYYEADTDSATKTFPNWMEPNW 122
Db 77 WISGNAQRIFVELKFTLRDCNSLPGLVGTCKETENLYYETDYD---TGRTNRENDLY 132
QY 123 KVDITAADEFSQVDLGGVVKMINTEVSRFGVPSRSGYFLAFQDYGGCMSLIAYRVFYRK 182
Db 133 KIDTIAADESFQDUGERKKMLNTEVREIGPLSKKGYFLAFQDVGACIALVSVKVYKK 192
QY 183 CPRIIQNGAIFQETLSGAESTSLVAARGSCIANA-EEVDVPIKLYCNGDGEWLVPIGRCM 241
Db 193 CWTIVENLAVPDTVTGSEFSSLYVEVRGTCVSSAEAEAFNSPRMHCSAEGEWLVPIGKCI 252
QY 242 CKAGFEAVENGTVG 255
Db 253 CKAGYQ--QKGDTC 264

RESULT 14
US-10-004-542-4
; Sequence 4, Application US/10004542
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Walke, D. Wade
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinase and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0260-USA
; CURRENT APPLICATION NUMBER: US/10/004,542
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/243,893
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 308
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-004-542-4

Query Match 15.1%; Score 771; DB 6; Length 308;
Best Local Similarity 55.9%; Pred. No. 2.9e-48;
Matches 162; Conservative 36; Mismatches 46; Indels 46; Gaps

QY 522 QEKLPLIIGSSAAGLVFLIADVVAIVCNR-RGFERADSEYTDKLO-HYTSGHIT-PGMK 578
Db 5 QGQILLVIATAAVGGFTLVLIVLTLFTITGRCQWYIKAKMKSEKRRNHLQNGHLRFPGK 64
QY 579 IYIDPTEDPDNEAVREFAKEIDISCVKIEQVIGAGEGVCSCGHLKLPKREIFVAIKT 638
Db 65 TYIDPTEDPSLVAHFEFAKEIDPSRIERVIGAGEGVCSCGRLKTPCKREIPVAIKT 124
QY 639 LKSGYTEKORRDFLSEASTMGQFDHPNVIHLEGVVTKST----- 677
Db 125 LKGGHMDRQRDFLEASTMGQFDHPNIIIRLVGVYTKSFPAIGVEAFPCPSFLRAGFLNS 184
QY 678 -----PVMITTEFMENGSLDSFLRQNDGQFTVIQLVGMRLGIAA 716

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Search completed: February 1, 2002, 10:00:07
Job time: 312 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: February 1, 2002, 09:53:00 ; Search time 192.18 Seconds
(without alignments)
1401.433 Million cell updates/sec

Title: US-09-378-759-11
Perfect score: 5116
Sequence: 1 LLAAVEETLMDTTATAEIG.....ILNSTQVMRAQNNQISVEV 970

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5116	100.0	970	8	US-08-449-645-11
2	5116	100.0	970	11	US-08-702-367-11
3	5116	100.0	970	17	US-09-378-759-11
4	5082	99.3	994	6	US-08-235-407-2
5	5082	99.3	994	11	US-08-727-463-2
6	5082	99.3	994	11	US-08-727-463-2
7	5082	99.3	994	11	US-08-730-700-2
8	5082	99.3	994	11	US-08-730-700-2
9	5082	99.3	994	20	US-09-621-595-2

10	3901.5	76.3	990	15	US-09-194-755A-7	Sequence 7, Appl1
11	3735	73.0	1009	3	US-07-861-390D-6	Sequence 6, Appl1
12	3632.5	71.0	998	8	US-08-449-645-20	Sequence 20, Appl
13	3632.5	71.0	998	11	US-08-702-367-20	Sequence 20, Appl
14	3632.5	71.0	998	17	US-09-378-759-20	Sequence 20, Appl
15	3632.5	71.0	1007	1	PCT-US01-03800A-2273	Sequence 2273, Ap
16	3631.5	71.0	999	24	US-60-201-702-172	Sequence 172, App
17	3590.5	70.2	993	19	US-09-558-340-1	Sequence 1, Appl1
18	3545.5	69.3	961	24	US-60-200-366-202	Sequence 202, App
19	3545.5	69.3	961	24	US-60-201-702-165	Sequence 165, App
20	3520.5	68.8	951	24	US-60-205-421-278	Sequence 278, App
21	3470	67.8	908	24	US-60-200-366-211	Sequence 211, App
22	3470	67.8	908	24	US-60-201-702-161	Sequence 161, App
23	3448.5	67.4	911	24	US-60-201-702-173	Sequence 173, App
24	3401	66.5	954	24	US-60-205-421-275	Sequence 275, App
25	3354	65.6	947	24	US-60-201-702-166	Sequence 166, App
26	3341.5	65.3	1002	15	US-09-194-755A-6	Sequence 6, Appl1
27	3292.5	64.4	889	24	US-60-201-702-162	Sequence 162, App
28	3289.5	64.3	905	24	US-60-205-421-289	Sequence 289, App
29	3031	59.2	953	21	US-09-751-389-7	Sequence 7, Appl1
30	3031	59.2	967	17	US-09-378-759-30	Sequence 30, Appl
31	3031	59.2	986	8	US-08-449-645-15	Sequence 15, Appl
32	3031	59.2	986	11	US-08-702-367-15	Sequence 15, Appl
33	3031	59.2	986	17	US-09-378-759-15	Sequence 13, Appl
34	3031	59.2	991	8	US-08-449-645-13	Sequence 13, Appl
35	3031	59.2	991	11	US-08-702-367-13	Sequence 13, Appl
36	3031	59.2	991	17	US-09-378-759-13	Sequence 13, Appl
37	3031	59.2	991	22	US-09-823-187-44	Sequence 44, Appl
38	3031	59.2	997	1	PCT-US01-08631-36048	Sequence 36048, A
39	3031	59.2	1026	1	PCT-US01-08631-53290	Sequence 53290, A
40	3026.5	59.2	993	22	US-09-823-187-39	Sequence 39, Appl
41	3026.5	59.2	993	22	US-09-823-187-41	Sequence 41, Appl
42	3024	59.1	1104	8	US-08-446-648-36	Sequence 36, Appl
43	3024	59.1	1104	11	US-08-770-449-36	Sequence 36, Appl
44	3016	59.0	998	8	US-08-449-645-17	Sequence 17, Appl
45	3016	59.0	998	11	US-08-702-367-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-449-645-11
; Sequence 11, Application US/08449645
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; APPLICANT: Welch, Andrew A.
; APPLICANT: Jing, Shugan
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645
; FILING DATE: May 24, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287-A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645-11

Query Match 100.0%; Score 5116; DB 8; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAAVEETLMDSTTATAGLWVHPSPGVEEVSVDENNTIRTYQVNCVFESSONNWL 60
Db 1 LLAAVEETLMDSTTATAGLWVHPSPGVEEVSVDENNTIRTYQVNCVFESSONNWL 60

QY 61 TKFIRRGARHIVHEMKFSVRDCSIPSPGCKTFNLYYEADFDATKTFPNNMENP 120
Db 61 TKFIRRGARHIVHEMKFSVRDCSIPSPGCKTFNLYYEADFDATKTFPNNMENP 120

QY 121 WYKVTIAADESFQVDLGGVRVKINTEVRSGPVSRSGLFADYDGCMSLIAVRVY 180
Db 121 WYKVTIAADESFQVDLGGVRVKINTEVRSGPVSRSGLFADYDGCMSLIAVRVY 180

QY 181 RKCPRIQNGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPIGR 240
Db 181 RKCPRIQNGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPIGR 240

QY 241 MCKAGFEAVENGTCVCGPSGTFKANGDEACTHCPINSRTTSEGATNCVCRNGYRADL 300
Db 241 MCKAGFEAVENGTCVCGPSGTFKANGDEACTHCPINSRTTSEGATNCVCRNGYRADL 300

QY 301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSSGGREDLVYNIICKSCSGRGACTR 360
Db 301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSSGGREDLVYNIICKSCSGRGACTR 360

QY 361 CGDNVOYAPQLGLTEPRYISDLAHTQYTFEIQAVNGVTDOFSPFCFASVNTTNOA 420
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Db 421 APSAVSIMHOVSRTVDSITLWSQDPOPNVILDYLOYYEKELSEYNATKSPNTVT 480

QY 481 GLKAGAIYVQVARTVAGYSGKMYFQTMTEAEYQTSIOEKLPLIIGSSAAGLVFLI 540
Db 481 GLKAGAIYVQVARTVAGYSGKMYFQTMTEAEYQTSIOEKLPLIIGSSAAGLVFLI 540

QY 541 AVVIAIVCNRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFYEDNEAVREFAKEI 600
Db 541 AVVIAIVCNRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFYEDNEAVREFAKEI 600

QY 601 DISCVKIEQVIGAGEGVCVSGHKLPGKREIFVAIKTLKSGYTEKQRIDFLSEASIMQ 660
Db 601 DISCVKIEQVIGAGEGVCVSGHKLPGKREIFVAIKTLKSGYTEKQRIDFLSEASIMQ 660

QY 661 FDNPNVHLBGVTKSTPVMITFEFENGSLDQFVQLVGMRLGIAAGMKY 720
Db 661 FDNPNVHLBGVTKSTPVMITFEFENGSLDQFVQLVGMRLGIAAGMKY 720

QY 721 LADNMYVHRDLAARNILVNSNLCKVSDGLSRFLEDSDTPTYSALGKFPRTAPE 780
Db 721 LADNMYVHRDLAARNILVNSNLCKVSDGLSRFLEDSDTPTYSALGKFPRTAPE 780

QY 781 AIOYRKFTSASVMSYGVIMVEMVMSYGERYWDNTQDVINAIEQDYRLPPMDCPALH 840
Db 781 AIOYRKFTSASVMSYGVIMVEMVMSYGERYWDNTQDVINAIEQDYRLPPMDCPALH 840

QY 841 QMLDCHQKDRNHRPKFGQIVNTLDKMRNPNSIKAMAPLSSGINPLDRTIPDVTSEN 900
Db 841 QMLDCHQKDRNHRPKFGQIVNTLDKMRNPNSIKAMAPLSSGINPLDRTIPDVTSEN 900

QY 901 TVDEWLEAIKMGQYKESFANAGETSFQVVSQMMEDILRVGVTLGAGHQKILNSIQMRA 960
Db 901 TVDEWLEAIKMGQYKESFANAGETSFQVVSQMMEDILRVGVTLGAGHQKILNSIQMRA 960

QY 961 QMNOIOSVEV 970
Db 961 QMNOIOSVEV 970

RESULT 2

US-08-702-367-11
Sequence 11, Application US/08702367
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION NUMBER: US/08/702,367
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,509
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367-11

Query Match 100.0%; Score 5116; DB 11; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAAVEETLMDSTTATAGLWVHPSPGVEEVSVDENNTIRTYQVNCVFESSONNWL 60
Db 1 LLAAVEETLMDSTTATAGLWVHPSPGVEEVSVDENNTIRTYQVNCVFESSONNWL 60

QY 61 TKFIRRGARHIVHEMKFSVRDCSIPSPGCKTFNLYYEADFDATKTFPNNMENP 120
Db 61 TKFIRRGARHIVHEMKFSVRDCSIPSPGCKTFNLYYEADFDATKTFPNNMENP 120

QY 121 WYKVTIAADESFQVDLGGVRVKINTEVRSGPVSRSGLFADYDGCMSLIAVRVY 180
Db 121 WYKVTIAADESFQVDLGGVRVKINTEVRSGPVSRSGLFADYDGCMSLIAVRVY 180

QY 181 RKCPRIQNGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPIGR 240
Db 181 RKCPRIQNGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPIGR 240

QY 241 MCKAGFEAVENGTCVCGPSGTFKANGDEACTHCPINSRTTSEGATNCVCRNGYRADL 300
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QY 841 QLMDCWQKDRHRPKFGQIVNTLDKMINRPNLSKAMAPLSSGINLPLDRTIPDYTSFN 900
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QY 961 QMNOIQSVEV 970
Db 961 QMNOIQSVEV 970

RESULT 3

US-09-378-759-11

; Sequence 11, Application US/09378759

; GENERAL INFORMATION:

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

; TITLE OF INVENTION: Kinases

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Angen Patent Operations/RBW

; STREET: 1840 Dehaviiland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/378.759

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/702.367

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-378-759-11

Query Match 100.0%; Score 5116; DB 17; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAAREETLMDSTATAELGWMVHPSPSGWEEVSGYDENNMNTIRTYQVCNVFESSQNNMLR 60
Db 1 LLAAREETLMDSTATAELGWMVHPSPSGWEEVSGYDENNMNTIRTYQVCNVFESSQNNMLR 60
QY 61 TKFIRRRGAHRIHVENKFSYRDCSSIPSPGSKETENLYYYEADFDSATKTFPNNMENP 120
Db 61 TKFIRRRGAHRIHVENKFSYRDCSSIPSPGSKETENLYYYEADFDSATKTFPNNMENP 120
QY 121 WKVDTIAADESFQVDLGGRVNKKINTEVRSFSPVSRSGFYLAQDYGCMSLIAVRVY 180
Db 121 WKVDTIAADESFQVDLGGRVNKKINTEVRSFSPVSRSGFYLAQDYGCMSLIAVRVY 180
QY 181 RKPRIQNGALFQETLSGAESTSLVAARGSCIANAEEDVPIKLYCNGDGEWLVPIGR 240
Db 181 RKPRIQNGALFQETLSGAESTSLVAARGSCIANAEEDVPIKLYCNGDGEWLVPIGR 240
QY 241 MCKAGFEAVENGTVCGCPSTGTFKANQGEACTHCPINRSRTTSEGATNCVCRNYYRADL 300
Db 241 MCKAGFEAVENGTVCGCPSTGTFKANQGEACTHCPINRSRTTSEGATNCVCRNYYRADL 300
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Db 301 DPLDMPCCTTISAPQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSGSGRGACTR 360
QY 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNTTNOA 420
Db 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNTTNOA 420
QY 421 APSAVSINHQSRTVDSITLSWSQDPPNGVILDYELQYERKELSEYNATAIKSPNTVT 480
Db 421 APSAVSINHQSRTVDSITLSWSQDPPNGVILDYELQYERKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYVFOVRARTVAGYGRYSGKMYFQTMTEAEYQTSIOEKLPLIGSSAAGLVFLI 540
Db 481 GLKAGAIYVFOVRARTVAGYGRYSGKMYFQTMTEAEYQTSIOEKLPLIGSSAAGLVFLI 540
QY 541 AVVYIAIVCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDPNEAVREFAKEI 600
Db 541 AVVYIAIVCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDPNEAVREFAKEI 600
QY 601 DISCVKIEQVIGAGEGECVSGHKLPGKREIFVAIKTLKSGYTEKQRDFLSEASIMQ 660
Db 601 DISCVKIEQVIGAGEGECVSGHKLPGKREIFVAIKTLKSGYTEKQRDFLSEASIMQ 660
QY 661 FDHPNVHLEGVVTKSTPVMIIITEPMENGSLDSFLRQNDGQFTVQLVGMRLGIAAGMKY 720
Db 661 FDHPNVHLEGVVTKSTPVMIIITEPMENGSLDSFLRQNDGQFTVQLVGMRLGIAAGMKY 720
QY 721 LADMNVYHRDLAARNILVNSNLVCKVDFGLSRLEDDTSDPTVTSALGGKFPRTAPE 780
Db 721 LADMNVYHRDLAARNILVNSNLVCKVDFGLSRLEDDTSDPTVTSALGGKFPRTAPE 780
QY 781 AIQYRKFTSASDVMSYGIWMVEVMSYGERPYWDMTNDQVINAIEDYRLPPMDCPSALH 840
Db 781 AIQYRKFTSASDVMSYGIWMVEVMSYGERPYWDMTNDQVINAIEDYRLPPMDCPSALH 840
QY 841 QLMDCWQKDRHRPKFGQIVNTLDKMINRPNLSKAMAPLSSGINLPLDRTIPDYTSFN 900
Db 841 QLMDCWQKDRHRPKFGQIVNTLDKMINRPNLSKAMAPLSSGINLPLDRTIPDYTSFN 900

Fri Feb 1 11:16:32 2002

us-09-378-759-11.rapm

Db 841 QLMDCWQKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSGINLPLDLRTIPDYTSN 900
Qy 901 TVDEWLEAIKMGQYKESFANAGTSTFDVVSQMMEDILRVGVTLAGHOKKILNSIQVMRA 960
Db 901 TVDEWLEAIKMGQYKESFANAGTSTFDVVSQMMEDILRVGVTLAGHOKKILNSIQVMRA 960
Qy 961 QMNOIQSVEV 970
Db 961 QMNOIQSVEV 970

RESULT 4
US-08-235-407-2
; Sequence 2, Application US/08235407
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; TITLE OF INVENTION: NOVEL NEURAL KINASE AND RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West, Box 401
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,407
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-82
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; TELEX: 06-23115
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Embryo
; IMMEDIATE SOURCE:
; LIBRARY: lambda gt10 cDNA library
; CLONE: Combined pNKRACE A2 and K2 and cDNA clones
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Distal end of chromosome 4
; MAP POSITION: near the ahd-1 mutation
US-08-235-407-2

Query Match 99.38; Score 5082; DB 6; Length 994;
Best Local Similarity 99.28; Pred. No. 0;
Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
Qy 1 LLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVPFESSQNNWLR 60
Db 23 LLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVPFESSQNNWLR 82
Qy 61 TKFIRRRGAHRIHVEMKFSVRDCSSIPSPGCKETFLNLYYYEADFSLATKTFPNNWENP 120

Db 83 TKFIRRRGAHRIHVEMKFSVRDCSSIPSPGCKETFLNLYYYEADFSLATKTFPNNWENP 142
Qy 121 WKVDTIAADSFQSDVLDGGRVMKINTEVRSFGPVSRSGFYLAQDYGGCMLIAVRVFF 180
Db 143 WKVDTIAADSFQSDVLDGGRVMKINTEVRSFGPVSRSGFYLAQDYGGCMLIAVRVFF 202
Qy 181 RKCPRILIONGALFOETLSGAESTSLVAARGSCIANAEEDVPIKLYCNGDGEWLVPIGR 240
Db 203 RKCPRILIONGALFOETLSGAESTSLVAARGSCIANAEEDVPIKLYCNGDGEWLVPIGR 262
Qy 241 MCKAGFEAVENGTVCRGCPSTGTFKANQGDGACTHCPINSRRTSEGATNCVCRNGYIRADL 300
Db 263 MCKAGFEAVENGTVCRGCPSTGTFKANQGDGACTHCPINSRRTSEGATNCVCRNGYIRADL 322
Qy 301 DPLDMPCCTTIPSAQAVISSVNETSLMLEWTTPRDSGGREDLVYNIICKSCGSGRGACTR 360
Db 323 DPLDMPCCTTIPSAQAVISSVNETSLMLEWTTPRDSGGREDLVYNIICKSCGSGRGACTR 382
Qy 361 CGDNVQYAPRQLGLTEPRIYISDILLAHTQYTFEIQAVNGVTDQSPFQFASVNTTNOA 420
Db 383 CGDNVQYAPRQLGLTEPRIYISDILLAHTQYTFEIQAVNGVTDQSPFQFASVNTTNOA 442
Qy 421 APSAVSIMHOVSRTVDSITLSWSQDPQNGVILDYELQYERKELSEYNATAIKSPNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLSWSQDPQNGVILDYELQYERKELSEYNATAIKSPNTVT 502
Qy 481 --GLKAGAIYVQVVRARTVAGYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVF 538
Db 503 VQGLKAGAIYVQVVRARTVAGYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVF 562
Qy 539 LIAVVVTAIVCNRRGFERADSEYTDKLOHVTSGHITPGMKIYIDPFTYEDPNEAVREFAK 598
Db 563 LIAVVVTAIVCNRRGFERADSEYTDKLOHVTSGHITPGMKIYIDPFTYEDPNEAVREFAK 622
Qy 599 EIDTSCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDRFLSEASIM 658
Db 623 EIDTSCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDRFLSEASIM 682
Qy 659 QOFDHPNVHLEGVVTYKSTPVMITFEMWNGSLDSFLRQNDGQFTVQLVGLMRLGIAAGM 718
Db 683 QOFDHPNVHLEGVVTYKSTPVMITFEMWNGSLDSFLRQNDGQFTVQLVGLMRLGIAAGM 742
Qy 719 KYLADMNVVRDLAARNILVNSLVCKVSDPGLSRFLSDDTSDPTYSALGGKPIRWTA 778
Db 743 KYLADMNVVRDLAARNILVNSLVCKVSDPGLSRFLSDDTSDPTYSALGGKPIRWTA 802
Qy 779 PEAIQYRKFTSASDVMSYGIWMVEVMSYGERPYWDMNQDVINAIEQDYRLPPMDCPSA 838
Db 803 PEAIQYRKFTSASDVMSYGIWMVEVMSYGERPYWDMNQDVINAIEQDYRLPPMDCPSA 862
Qy 839 LHQLMDCWQKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSGINLPLDLRTIPDYTS 898
Db 863 LHQLMDCWQKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSGINLPLDLRTIPDYTS 922
Qy 899 FNTVDENLEAIKMGQYKESFANAGTSTFDVVSQMMEDILRVGVTLAGHOKKILNSIQVM 958
Db 923 FNTVDENLEAIKMGQYKESFANAGTSTFDVVSQMMEDILRVGVTLAGHOKKILNSIQVM 982
Qy 959 RAQMNOIQSVEV 970
Db 983 RAQMNOIQSVEV 994

RESULT 5
US-08-727-463-2
; Sequence 2, Application US/08727463
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; APPLICANT: Letwin, Kenneth
; TITLE OF INVENTION: NEURAL RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: MERCHANT & GOULD
STREET: 3100 Northwest Center, 90 South Seventh Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: U.S.A.
ZIP: 55403-4131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/08-727,463
FILING DATE: 18-OCT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: M&G 7933.89-US-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 332-5300
TELEFAX: (612) 332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:
LIBRARY: lambda gt10 cDNA library
CLONE: Combined pNURKE A2 and K2 and cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Distal end of chromosome 4
MAP POSITION: near the ahd-1 mutation
US-08-727-463-2

Query Match 99.3%; Score 5082; DB 11; Length 994;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 LLAVEETLMDSTTATAELGVMVHPFSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLR 60
Db 23 LLAVEETLMDSTTATAELGVMVHPFSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLR 82
Qy 61 TKFTRRGARRHIVEMKFSYRDCSSIPSPGCKETFLNLYYEADFDATKTPNNMNP 120
Db 83 TKFTRRGARRHIVEMKFSYRDCSSIPSPGCKETFLNLYYEADFDATKTPNNMNP 142
Qy 121 WKVYDTTAADESFQVLGGRVVKINTEVRSFGVPSRSGFYLAQDYGCMGLIAYRVFY 180
Db 143 WKVYDTTAADESFQVLGGRVVKINTEVRSFGVPSRSGFYLAQDYGCMGLIAYRVFY 202
Qy 181 RKCPRIITQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPVIGRC 240
Db 203 RKCPRIITQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPVIGRC 262
Qy 241 MCRAGFEAVENGTVCRGCPSTGTFKANGQDEACTHCIPNSRTTSEGATNCVCRNGYTRDL 300
Db 263 MCRAGFEAVENGTVCRGCPSTGTFKANGQDEACTHCIPNSRTTSEGATNCVCRNGYTRDL 322
Qy 301 DPLDMPCTTTPSAQAVISSVNETSLMLEWTPPRSGGREDLVYNIICKSCGSGRGACTR 360
Db 323 DPLDMPCTTTPSAQAVISSVNETSLMLEWTPPRSGGREDLVYNIICKSCGSGRGACTR 382
Qy 361 CGNVQYAPRQLGLTEPRYIISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 420
Db 383 CGNVQYAPRQLGLTEPRYIISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 442

Qy 421 APSAVSINHQSRTVDSITLSWSQDOPNGVILDYELQYVEKELSEYNATAIKSPNTVT 480
Db 443 APSAVSINHQSRTVDSITLSWSQDOPNGVILDYELQYVEKELSEYNATAIKSPNTVT 502
Qy 481 --GLKAGAIYVQVRARTVAGYSGMYFQMTAEYQTSIOEKPLIIGSSAAGLVF 538
Db 503 VOGLKAGAIYVQVRARTVAGYSGMYFQMTAEYQTSIOEKPLIIGSSAAGLVF 562
Qy 539 LIAVVVIAIYCNRRGFERADSEYTDKLOHTYSGHITPGMKIYIDPFTYEDPNEAVREFAK 598
Db 563 LIAVVVIAIYCNRRGFERADSEYTDKLOHTYSGHITPGMKIYIDPFTYEDPNEAVREFAK 622
Qy 599 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSEASIM 658
Db 623 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSEASIM 682
Qy 659 GQPDHPNVHLEGVVTKSTPVMITTEFMENGSLDSEFLRQNDGQFTVQLVGLRGIAAGM 718
Db 683 GQPDHPNVHLEGVVTKSTPVMITTEFMENGSLDSEFLRQNDGQFTVQLVGLRGIAAGM 742
Qy 719 KYLADNMVYHRDLAARNILVNSLVCKVSDGFLSRELEDDTSDPTTYSALGKGFPIRWTA 778
Db 743 KYLADNMVYHRDLAARNILVNSLVCKVSDGFLSRELEDDTSDPTTYSALGKGFPIRWTA 802
Qy 779 PEAIQYRKFTSASDVNSYGIYVMEVMSYGERPYWDMTNDQVINAIBODYRLPPMDCPSA 838
Db 803 PEAIQYRKFTSASDVNSYGIYVMEVMSYGERPYWDMTNDQVINAIBODYRLPPMDCPSA 862
Qy 839 LHQLMLDCQKORNRHPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLDRTIPDVTYS 898
Db 863 LHQLMLDCQKORNRHPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLDRTIPDVTYS 922
Qy 899 FNTVDEWLEAIKMGQYKESFANAGFTSFQVWSOMMEDILRVGVTLAGHOKKILNSIQVM 958
Db 923 FNTVDEWLEAIKMGQYKESFANAGFTSFQVWSOMMEDILRVGVTLAGHOKKILNSIQVM 982
Qy 959 RAQMNOIQSVEV 970
Db 983 RAQMNOIQSVEV 994

RESULT 6
US-08-727-463-2
; Sequence 2, Application US/08727463A
; GENERAL INFORMATION:
; APPLICANT: PAWSON, ANTHONY
; APPLICANT: HENKEMEYER, MARK
; APPLICANT: LETWIN, KENNETH
; APPLICANT: MOUNT SINAI HOSPITAL CORPORATION
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SUBSTANCES AFFECTING RECEPTOR
; TITLE OF INVENTION: TITROSINE KINASE ACTIVITY (AS AMENDED)
; FILE REFERENCE: 7933.89USWO
; CURRENT APPLICATION NUMBER: US/08/727,463A
; CURRENT FILING DATE: 1997-03-11
; EARLIER APPLICATION NUMBER: PCT/CA95/00254
; EARLIER FILING DATE: 1995-04-28
; EARLIER APPLICATION NUMBER: 08/235,407
; EARLIER FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 994
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-727-463-2

Query Match 99.3%; Score 5082; DB 11; Length 994;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 LLAVEETLMDSTTATAELGVMVHPFSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLR 60

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Db	23	LLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLR	82
QY	61	TKFIRRRGAHRHIVEMKFSVRDCSSIPSPGSKCTFNLYYYEADFSAKTFPNNMENP	120
Db	83	TKFIRRRGAHRHIVEMKFSVRDCSSIPSPGSKCTFNLYYYEADFSAKTFPNNMENP	142
QY	121	WKVDTIAADESFQVDLGGVRMKINTVRSFGVSRSGFYLAFOYGGCMSLIAVRVY	180
Db	143	WKVDTIAADESFQVDLGGVRMKINTVRSFGVSRSGFYLAFOYGGCMSLIAVRVY	202
QY	181	RKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGLWLPIGRC	240
Db	203	RKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGLWLPIGRC	262
QY	241	MCKAGFEAVENGTVCRGCPSTGTFKANQGDGACTHCPINSRTTSEGATNCVCRNGYRADL	300
Db	263	MCKAGFEAVENGTVCRGCPSTGTFKANQGDGACTHCPINSRTTSEGATNCVCRNGYRADL	322
QY	301	DLDPMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR	360
Db	323	DLDPMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR	382
QY	361	CGDNVOYAPROLGLETPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSQFASVNIITNOA	420
Db	383	CGDNVOYAPROLGLETPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSQFASVNIITNOA	442
QY	421	APSAVSIHQVSTVDISITLSWSQDPQNGVILDYQYKELSEYNATAIKSPNTVT	480
Db	443	APSAVSIHQVSTVDISITLSWSQDPQNGVILDYQYKELSEYNATAIKSPNTVT	502
QY	481	--GLKAGAIYVFOVRTVAGYGRYSGKMYFQMTAEYQTSIOEKLPLIGSSAAGLVF	538
Db	503	VQGLKAGAIYVFOVRTVAGYGRYSGKMYFQMTAEYQTSIOEKLPLIGSSAAGLVF	562
QY	539	LIWVVIATVNCNRGERADSEYTDKQHYTSGHLPKMKIYIDPTYEDPNEAVREFAK	598
Db	563	LIWVVIATVNCNRGERADSEYTDKQHYTSGHLPKMKIYIDPTYEDPNEAVREFAK	622
QY	599	EIDISCVKIEQVIGAGFGEVCSGHLKPKGREIFVAIKTLKSGYTEKORRDFLSEASIM	658
Db	623	EIDISCVKIEQVIGAGFGEVCSGHLKPKGREIFVAIKTLKSGYTEKORRDFLSEASIM	682
QY	659	GQDPHPNVIHLEGVYKSTPVMIIITFPMENGSLDSTLRQNDGQFTVIQJVGMLRGAAGM	718
Db	683	GQDPHPNVIHLEGVYKSTPVMIIITFPMENGSLDSTLRQNDGQFTVIQJVGMLRGAAGM	742
QY	719	KYLADMNVVRHDLAARNILVNSNLCKVSDFGLSRFLSDPTSTYTSALGGKPIRWTA	778
Db	743	KYLADMNVVRHDLAARNILVNSNLCKVSDFGLSRFLSDPTSTYTSALGGKPIRWTA	802
QY	779	PEAIQYRKFTSASDVWSYGVIMVEVNSYGERPYWDMTNQDVINAIBODYRLPPMDCPSA	838
Db	803	PEAIQYRKFTSASDVWSYGVIMVEVNSYGERPYWDMTNQDVINAIBODYRLPPMDCPSA	862
QY	839	LHQLMDCQKDRNRPKFGQIVNTLQKMRNPNLSKAMAPLSGGINLPDLRTIPDYS	898
Db	863	LHQLMDCQKDRNRPKFGQIVNTLQKMRNPNLSKAMAPLSGGINLPDLRTIPDYS	922
QY	899	FNTVDEWLEAIKMGQYKESFANAGTSTFVVVSQMMEDILRVGYTLGAGHOKKILNSIQVM	958
Db	923	FNTVDEWLEAIKMGQYKESFANAGTSTFVVVSQMMEDILRVGYTLGAGHOKKILNSIQVM	982
QY	959	RAQMNQIOSVEV 970	
Db	983	RAQMNQIOSVEV 994	
RESULT 7			
US-08-730-700-2			
; Sequence 2, Application US/08730700			
; GENERAL INFORMATION:			
; APPLICANT: Pawson, Anthony			
; APPLICANT: Henkemeyer, Mark			
; TITLE OF INVENTION: Method of Activating a Novel Ligand			
; TITLE OF INVENTION: Regulatory Pathway			
; NUMBER OF SEQUENCES: 2			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Bereskin & Parr			
; STREET: 40 King Street West, Box 401			
; CITY: Toronto			
; STATE: Ontario			
; COUNTRY: Canada			
; ZIP: M5H 3Y2			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/730,700			
; FILING DATE:			
; CLASSIFICATION: 424			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Kurdydyk, Linda M.			
; REGISTRATION NUMBER: 34,971			
; REFERENCE/DOCKET NUMBER: 3153-197			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (416) 364-7311			
; TELEFAX: (416) 361-1398			
; TELEX: 06-23115			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 994 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; ORIGINAL SOURCE:			
; ORGANISM: Mus musculus			
; DEVELOPMENTAL STAGE: Embryo			
; IMMEDIATE SOURCE:			
; LIBRARY: lamda gt10 cDNA library			
; CLONE: Combined pNukRACE A2 and K2 and cDNA clones			
; POSITION IN GENOME:			
; CHROMOSOME/SEGMENT: Distal end of chromosome 4			
; MAP POSITION: near the and-1 mutation			
US-08-730-700-2			
Query Match 99.3%; Score 5082; DB 11; Length 994;			
Best Local Similarity 99.2%; Pred. No. 0;			
Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;			
QY	1	LLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLR	60
Db	23	LLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLR	82
QY	61	TKFIRRRGAHRHIVEMKFSVRDCSSIPSPGSKCTFNLYYYEADFSAKTFPNNMENP	120
Db	83	TKFIRRRGAHRHIVEMKFSVRDCSSIPSPGSKCTFNLYYYEADFSAKTFPNNMENP	142
QY	121	WKVDTIAADESFQVDLGGVRMKINTVRSFGVSRSGFYLAFOYGGCMSLIAVRVY	180
Db	143	WKVDTIAADESFQVDLGGVRMKINTVRSFGVSRSGFYLAFOYGGCMSLIAVRVY	202
QY	181	RKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGLWLPIGRC	240
Db	203	RKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGLWLPIGRC	262
QY	241	MCKAGFEAVENGTVCRGCPSTGTFKANQGDGACTHCPINSRTTSEGATNCVCRNGYRADL	300
Db	263	MCKAGFEAVENGTVCRGCPSTGTFKANQGDGACTHCPINSRTTSEGATNCVCRNGYRADL	322
QY	301	DLDPMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR	360

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Db 323 DPLDMPCITIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR 382
Qy 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 420
Db 383 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 442
Qy 421 APSAVSIMHOVSRTVDSITLSWSQDPQNGVILDYELQYIEKELSEYNATAIKSPTNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLSWSQDPQNGVILDYELQYIEKELSEYNATAIKSPTNTVT 502
Qy 481 --GLKAGAIYVFOVRARTVAGYRGYSGKMYFQTMTEAETYSIOEKLPIITGSSAAGLVF 538
Db 503 VQGLKAGAIYVFOVRARTVAGYRGYSGKMYFQTMTEAETYSIOEKLPIITGSSAAGLVF 562
Qy 539 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAVREFAK 598
Db 563 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAVREFAK 622
Qy 599 EIDISCVKIEQVIGAGEGVCVSGHLKLPGRKREIFVAIKTLKSGYTEKQRDRFLSEASIM 658
Db 623 EIDISCVKIEQVIGAGEGVCVSGHLKLPGRKREIFVAIKTLKSGYTEKQRDRFLSEASIM 682
Qy 659 GQFDHPNVHLEGVVTSTPVMIIITEFMENGLDSFLRQNDGQFTVIQLVGMRLGIAAGM 718
Db 683 GQFDHPNVHLEGVVTSTPVMIIITEFMENGLDSFLRQNDGQFTVIQLVGMRLGIAAGM 742
Qy 719 KYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTTYSALGGKFPPIRWTA 778
Db 743 KYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTTYSALGGKFPPIRWTA 802
Qy 779 PEATQYRKFTSASDVWSGVIMVEMVSGYGRPYWDMTNDQVINAEQDYRLPPMDCPSA 838
Db 803 PEATQYRKFTSASDVWSGVIMVEMVSGYGRPYWDMTNDQVINAEQDYRLPPMDCPSA 862
Qy 839 LHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPDLDRTPIDYTS 898
Db 863 LHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPDLDRTPIDYTS 922
Qy 899 FNTVDEWLEAIKMGQYKESFANAGFTSFDFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 958
Db 923 FNTVDEWLEAIKMGQYKESFANAGFTSFDFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 982
Qy 959 RAQNMNQISQVEV 970
Db 983 RAQNMNQISQVEV 994
```

RESULT 8

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US-08-730-700A-2
; Sequence 2, Application US/08730700A
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; TITLE OF INVENTION: Method of Activating a Novel Ligand
; TITLE OF INVENTION: Regulatory Pathway
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Room 970
; STREET: 600 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1X5
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,700A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 60/005,518
; FILING DATE: 13-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurydyk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 416-586-3235
; TELEFAX: 416-586-3110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-730-700A-2
```

```
Query Match 99.3%; Score 5082; DB 11; Length 994;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 LLAAVEETLMDSTTATAELGWMVHPSPSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLR 60
Db 23 LLAAVEETLMDSTTATAELGWMVHPSPSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLR 82
Qy 61 TKFIRRGAAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSDATKTFPNNMNP 120
Db 83 TKFIRRGAAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSDATKTFPNNMNP 142
Qy 121 WKVDTIAADESFQVDLGGRYMKINTEVRSRGPVSRSGFYLAFOYDGCMSLIAVRVYF 180
Db 143 WKVDTIAADESFQVDLGGRYMKINTEVRSRGPVSRSGFYLAFOYDGCMSLIAVRVYF 202
Qy 181 RKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEEDVDPIKLYCNGDGMWLPICRC 240
Db 203 RKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEEDVDPIKLYCNGDGMWLPICRC 262
Qy 241 MCKAGFEAVENGTCVRCGCPSTGTFKANQDEACTHCPINSTRTSEGATNCVCRNGYRADL 300
Db 263 MCKAGFEAVENGTCVRCGCPSTGTFKANQDEACTHCPINSTRTSEGATNCVCRNGYRADL 322
Qy 301 DPLDMPCITIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR 360
Db 323 DPLDMPCITIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR 382
Qy 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 420
Db 383 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 442
Qy 421 APSAVSIMHOVSRTVDSITLSWSQDPQNGVILDYELQYIEKELSEYNATAIKSPTNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLSWSQDPQNGVILDYELQYIEKELSEYNATAIKSPTNTVT 502
Qy 481 --GLKAGAIYVFOVRARTVAGYRGYSGKMYFQTMTEAETYSIOEKLPIITGSSAAGLVF 538
Db 503 VQGLKAGAIYVFOVRARTVAGYRGYSGKMYFQTMTEAETYSIOEKLPIITGSSAAGLVF 562
Qy 539 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAVREFAK 598
Db 563 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAVREFAK 622
Qy 599 EIDISCVKIEQVIGAGEGVCVSGHLKLPGRKREIFVAIKTLKSGYTEKQRDRFLSEASIM 658
Db 623 EIDISCVKIEQVIGAGEGVCVSGHLKLPGRKREIFVAIKTLKSGYTEKQRDRFLSEASIM 682
Qy 659 GQFDHPNVHLEGVVTSTPVMIIITEFMENGLDSFLRQNDGQFTVIQLVGMRLGIAAGM 718
Db 683 GQFDHPNVHLEGVVTSTPVMIIITEFMENGLDSFLRQNDGQFTVIQLVGMRLGIAAGM 742
Qy 719 KYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTTYSALGGKFPPIRWTA 778
Db 743 KYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTTYSALGGKFPPIRWTA 802
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Db	743	KYLAADNVVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSALGGKIPIRWTA	802
Qy	779	PEAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNODVINAIEQDYELPPPMDCPSA	838
Db	803	PEAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNODVINAIEQDYELPPPMDCPSA	862
Qy	839	LHQLMDCQKDRNHRPKFGQIVNTLDMIRNPNSLKAMAPLSSGINPLDRTIPDYS	898
Db	863	LHQLMDCQKDRNHRPKFGQIVNTLDMIRNPNSLKAMAPLSSGINPLDRTIPDYS	922
Qy	899	ENTVDEWLEAKMGQYKESFANAGFTSFDVVSOMMEDILRVGVTLAGHOKKILNSIQVM	958
Db	923	ENTVDEWLEAKMGQYKESFANAGFTSFDVVSOMMEDILRVGVTLAGHOKKILNSIQVM	982
Qy	959	RAQMNIQISVEV 970	
Db	983	RAQMNIQISVEV 994	
RESULT: 9			
US-09-621-595-2			
; Sequence 2, Application US/09621595			
; GENERAL INFORMATION:			
; APPLICANT: Pawson, Anthony			
; TITLE OF INVENTION: Method of Activating a Novel Ligand			
; Regulatory Pathway			
; NUMBER OF SEQUENCES: 21			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Room 970			
; STREET: 600 University Avenue			
; CITY: Toronto			
; STATE: Ontario			
; COUNTRY: Canada			
; ZIP: M5G 1X5			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/621,595			
; FILING DATE: 21-Jul-2000			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/730,700			
; FILING DATE: <Unknown>			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Kurdydyk, Linda M.			
; REGISTRATION NUMBER: 34,971			
; REFERENCE/DOCKET NUMBER: 3153-196			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 416-586-3235			
; TELEFAX: 416-586-3110			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 994 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
US-09-621-595-2			
Query Match 99.3%; Score 5082; DB 20; Length 994;			
Best Local Similarity 99.2%; Pred. No. 0;			
Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;			
Qy	1	LLAAVEETLMDSTATAELGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNWL	60
Db	23	LLAAVEETLMDSTATAELGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNWL	82
; APPLICANT: Matsui, Toshimitsu			
; TITLE OF INVENTION: Novel Human Receptor Type Tyrosine			
; KINASES LIKE PROTEIN			
; FILE REFERENCE: 07541.0001-00000			

RESULT 10
US-09-194-755A-7
; Sequence 7, Application US/09194755A
; GENERAL INFORMATION:
; APPLICANT: Matsui, Toshimitsu
; TITLE OF INVENTION: Novel Human Receptor Type Tyrosine
; KINASES LIKE PROTEIN
; FILE REFERENCE: 07541.0001-00000

; CURRENT APPLICATION NUMBER: US/09/194,755A
 ; PRIOR FILING DATE: 1999-04-14
 ; PRIOR APPLICATION NUMBER: PCT/JP97/01887
 ; PRIOR FILING DATE: 1997-06-04
 ; PRIOR APPLICATION NUMBER: JP 141849/1996
 ; PRIOR FILING DATE: 1996-06-04
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 990
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-194-755A-7

Query Match 76.3%; Score 3901.5; DB 15; Length 990;
 Best Local Similarity 73.5%; Pred. No. 4.2e-272;
 Matches 717; Conservative 128; Mismatches 121; Indels 9; Gaps 3;

QY 2 LAAVEETLMDSTTATAEGLGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRT 61
 DB 15 VAAEETLMDTRTATAEGLGMVHPSPGWEVSGYDENMNTIRTYQVCNVFEPQNNWLLT 74
 QY 62 KTRRGGAIRHIVEMKFSVRDCSSIPSVCCKETENLYYYEADFSATKTFPNNWENPW 121
 DB 75 TFINRRGAIRIYTEMFTVRDCSSLPNVPSCKETENLYYYETDSVIATKKSFAWSEAPY 134
 QY 122 VKVDTTAADESES-----QVDLGGVRMINTVRFPGVPSRSGFYLAFQDYGCGMSLIA 175
 DB 135 LKVDTTAADESSSSAAQVDFGGRLMKVNTVRFGLTRNGFYLAFQDYGACHSLLS 194
 QY 176 VRVYRKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWLV 235
 DB 195 VRVYRKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWLV 254
 QY 236 PIGRCMCKAGFAVENGVYVCRGCPSTFKANQGEACTHCPIINSTRTSEGATNCVCRNGY 295
 DB 255 PIGRCMCKAGFAVENGVYVCRGCPSTFKANQGEACTHCPIINSTRTSEGATNCVCRNGY 313
 QY 296 YRADLPLDMPCTTISAPQAVISSVNETSLMLETTPRDSGREDLVNITCKSGSQR 355
 DB 314 YRADLPLDMPCTTISAPQAVISSVNETSLMLETTPRDSGREDLVNITCKSGSQR 373
 QY 356 GACTRCGDNVQAPRGLGTPEPRYISDLSLAHTOYFEIQAVNGVTDQSPFSPQFASVNI 415
 DB 374 RSCRCDDNVQAPRGLGTPEPRYISDLSLAHTOYFEIQAVNGVTDQSPFSPQFASVNI 433
 QY 416 TTNQAAPSVMHQSATMRSITLSMPQEPQNGIILDEYIERYEKEHNEFNSSMARSQ 475
 DB 434 TTNQAAPSVMHQSATMRSITLSMPQEPQNGIILDEYIERYEKEHNEFNSSMARSQ 493
 QY 476 TWT--VTGLKAGAIYVQVARTVAGYGRYSKMYQTMTEAYQTSIOEKPLIIGSSA 533
 DB 494 TWTARIDGLRPGMVVYVQVARTVAGYGRYSKMYQTMTEAYQTSIOEKPLIIGSSA 553
 QY 534 AGVFLIIVVTAIVCNRRGERADSEYDKLOHYTSGHITFCMKIYIDPFYEDPNEAV 593
 DB 554 AGVFLIIVVTAIVCNRRGERADSEYDKLOHYTSGHITFCMKIYIDPFYEDPNEAV 613
 QY 594 REFKAIDISCVKIEQVIGAGFEGVCSGHLKLPGRKEIFVAIKTLKSGVTEKORDELS 653
 DB 614 REFKAIDISCVKIEQVIGAGFEGVCSGHLKLPGRKEIFVAIKTLKSGVTEKORDELS 673
 QY 654 EASIMQFDPHNVHLEGVVYVTKSTPVMITFPMENGLSFLRQNDGQFTVQLVGLMRG 713
 DB 674 EASIMQFDPHNVHLEGVVYVTKSTPVMITFPMENGLSFLRQNDGQFTVQLVGLMRG 733
 QY 714 IAAGMKYLADMYVHRDLAARILVNSLVCKVSDPGLSRFLEDDTSDTYTSALGCKFP 773
 DB 734 IAAGMKYLADMYVHRDLAARILVNSLVCKVSDPGLSRFLEDDTSDTYTSALGCKFP 793
 QY 774 IRWTAPEAIYRKFTSASDVWSYGVIMVWMSYGERPYWDMTNOQVINAIEODYRLPPPM 833

DB 794 VRWTAPEAIYRKFTSASDVWSYGVIMVWMSYGERPYWDMTNOQVINAIEODYRLPPPM 853
 QY 834 DCPALHQLMDCWOKDRHPRKFGOIVNTLDMKMINPSLAKAMAPLSSGINPLLDRTI 893
 DB 854 DCPALHQLMDCWOKDRHPRKFGOIVNTLDMKMINPSLAKAMAPLSSGINPLLDRTI 913
 QY 894 PDYTSNTVDLEAIAKMGQYKESFANAGTSPDVYSOMMEDILRVGTLAGHOKKILN 953
 DB 914 PDYTSNTVDLEAIAKMGQYKESFANAGTSPDVYSOMMEDILRVGTLAGHOKKILN 973
 QY 954 SIQVMRAQMNQISQV 968
 DB 974 SIHSMRVQMNQISQV 988

RESULT 11
 US-07-861-390D-6
 ; Sequence 6, Application US/07861390D
 ; GENERAL INFORMATION:
 ; APPLICANT: PAWSON et al.
 ; TITLE OF INVENTION: METHOD FOR EXPRESSING A
 ; TITLE OF INVENTION: PHOSPHORYLATED PROTEIN
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Linda M. Kurdydyk, Bereskin & Parr
 ; STREET: 40 King Street West, P. O. Box 401
 ; CITY: Toronto, Ontario
 ; STATE: N/A
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: DOS Text File
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/861,390D
 ; FILING DATE: 19920331
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: J.G. Mullins
 ; REGISTRATION NUMBER: 33073
 ; REFERENCE/DOCKET NUMBER: 027-021
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 684-1111
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1009 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-07-861-390D-6

Query Match 73.0%; Score 3735; DB 3; Length 1009;
 Best Local Similarity 71.3%; Pred. No. 4.5e-260;
 Matches 708; Conservative 129; Mismatches 130; Indels 26; Gaps 13;

QY 2 LAAVEETLMDSTTATAEGLGMVHP-PSGWEVSGYDENMNTIRTYQVCNV-PESSQNNML 59
 DB 15 VAAEETLMDTRTATAEGLGMVHPXASGWEVSGYDENLNTIRTYQVCNVXEPQNNML 74
 QY 60 RTKFIIRRRG-AHRIHVEMKFSVRDCSSIPSVP--GSKETFNLYYYEADFSATKTFPNN 116
 DB 75 LTFINRRGAIRIYTEMFTVRDCSSLPNVPXGSKETFNLYYYEADFSATKTFPNN 134
 QY 117 MENPVKVDITAADESFSDVLDGGRVWKINTEVRSPGVSRSGFYLAFQDYGCGMSLIAV 176
 DB 135 SEAPYLVKDIIAADESFSDVLDGGRVWKINTEVRSPGVSRSGFYLAFQDYGCGMSLIAV 194
 QY 177 RVYRKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVDP---IKLYCNGDGEM 233

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Db 195 RVFFKCPISVQNFVFAPEINTGAESTSLVIARTGTCIPNAEVDVPPXXXIKLXNGDGEW 254
QY 234 LVPTGRCMKAGAEVNGVTCGCPSTGKANOQDEACTHCPINSTRTTSEGTATNCVCRN 293
Db 255 WPIGRTCTKAGYEPENXVACACAGTGTASQAEAGCSHCPSNSRSPSEASPICTCRT 314
QY 294 GYRADLDPLDMPCTTTPSAPOAVISSV-NETSLMLEWTTPROSGGREDIVYNIICKSCG 352
Db 315 GYRADLDPPEVACTSVPSGRNVISVXNETSILLEHHPHRETGGRDDTYNIICKKX 374
QY 353 SGRG---ACTRCGDNVOYAPRQLGLTEPRYIISDLAHTQYTFEIQAVNGVTDOSPSPQ 409
Db 375 XNRADRSRCDNDNEFVRQLGLTECRVSIISLWHTPTFTDQIAINGVSSKSPFPQ 434
QY 410 -FASVNTTNOAAPSIVSIHMO-VSRVDSITLSWSQDOPNGVILDYQYXKELSEY 467
Db 435 HVXSVNTTNOAAPTVPIMHGXVSATMRSTLSWPOEQPNGLIILDIETIYXKEHNEF 494
QY 468 NATAIKSPINT--VTGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIOEKL 525
Db 495 NSSWARSQTNARIDGLRPGVYVQVARIAGYGRFGSKMCFQTLTDIDYKSELREL 554
QY 526 PLITGSSAAGLVFLIIVVIAVNCNRGFERADSEYTDK-----LQHTSCHIITPGMKIYI 581
Db 555 PLIAGSAAAGVVFVSVLAISIVGSRKRAYSKAAYSDKXXXLQHYSTCRGSPGMKIYI 614
QY 582 DPFTYEDPNEAVREFAKEIDISCV-----KIEQVIGAGEFGEVCSGHLKLP-KREIFVA 635
Db 615 DPFIYEDPNEAVREFAKEIDVSFYVXXXXKIEEVIGAGEFGEVYKRLKIPGXKREIYVA 674
QY 636 IKTLKSGYTEKQRDFTLSEASIMQFQDHPNVHLEGVVTKSTPTVMIITEFMENGLSDFL 695
Db 675 IKILKAGYSEKQRDFTLSEASIMQFQDHPNIIRLEGVVTKSRPVMIIITEFMENGALDSFL 734
QY 696 RQNDQFTVITOLVGLMGRGIAAGMKYLADNMVVRHDLAARNILVNSLVCKYVSDFLGREL 755
Db 735 RONDEQFTVITOLVGLMGRGIAAGMKYLSMNIVVRHDLAARNILVNSLVCKYVSDFLGREL 794
QY 756 EDDTSDPTYSALGKFPRTWTAPEATQYRFTSASDVMSYGIWVWVMSYGERPYWDMT 815
Db 795 QDDTSDPTYSALGKFPRTWTAPEATQYRFTSASDVMSYGIWVWVMSYGERPYWDMS 854
QY 816 NQDVINAIEQDYLPPPMDCPSALHQLMDCQKDRNHRPFQGOIVNTLDMIRNPNSLK 875
Db 855 NQDVINAIEQDYLPPPMDCPSALHQLMDCQKDRNHRPFQGOIVNTLDMIRNPNSLK 914
QY 876 AMAPLSSGINPLDRTIPDYTSFNTDNLWLEATKMGYKESFANAGFTSPDVVSOMME 935
Db 915 TVATITAVPSQPLLDRTIPDYTSFNTDNLWLEATKMGYKESFANAGFTSPDVVSOMME 974
QY 936 DILRVGVTLACHQKILNSIOVMRAQMNQISV 968
Db 975 DLLRIGVTLACHQKILNSIOVMRAQMNQISV 1007

```

RESULT 12

US-08-449-645-20

Sequence 20, Application US/08449645

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

APPLICANT: Welcher, Andrew A.

APPLICANT: Jing, Shuguan

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESS: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645
; FILING DATE: May 24, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287-A
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645-20

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Query Match 71.0% Score 3632.5; DB 8; Length 998;

Best Local Similarity 70.5% Pred. No. 11e-252;

Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

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QY 4 AVEETLMDSTTATLAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKF 63
Db 37 ALEETLMDTKVWTSELAWTSHPSGWEVSGYDEAMNPRTYQVCNVFESSQNNWLRTGF 96
QY 64 IRRGGAHRIHVMFVSVDYCSIPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKF 123
Db 97 IWRDVRVVYVELAFTVRDCNSIPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKF 156
QY 124 VDTAADESFSQVLDGGRVVKINTEVRSFGVSRGFLAFQDYGGCMSLIARVRYRKC 183
Db 157 VDTAPDESFLDAG---RVNTKVSFGPLSRAGFLAFQDQGACNSLISVAFYKCC 212
QY 184 PRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPGRCKMCK 243
Db 213 ASATGAFALFETLTGAEPTSLVIAAGTCIPNAVEVSPLKLYCNGDGEWMPVAGACTCA 272
QY 244 AGFEAVENGTVCRGCPGCTFKANOGDEACTHCPINSTRTTSEGTATNCVCRNVLRLDPL 303
Db 273 TGHPAKESOCRCPPGSGYKAKOGEGCLPCPNSTRTTSPAASICTCHNNFYRADSDSA 332
QY 304 DMPCTTIPSAQAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSC--GSGRGACTRC 361
Db 333 DSACTTVPSPRGVSNVNETSLILEWSEPRDLGVDRDLYNVICKCKHAGGASACSRK 392
QY 362 GDNVOYAPRQLGLTEPRYIISDLAHTQYTFEIQAVNGVTDOSPSPQFASVNTTNOAA 421
Db 393 DDNVEFVRQLGLSEPRVHTSHLLAHTRYTTEVOAVNGVSGKSPPLPPRYAAVNTTNOAA 452
QY 422 PSVSIHQVSRVDSITLSWSQDOPNGVILDYQYXKELSEYNATAIKSPNTV-- 479
Db 453 PSEVPTLRLHSSGSSSLTWAPERPNGVILDYEMKIFER--SEGIASTVTSQNNVQL 510
QY 480 TGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAE-AYQTSIOEKLPLIIGSSAAGLVF 538
Db 511 DGLRDPARYVQVARTVAGYGRYSGKMYFQMTAE-AYQTSIOEKLPLIIGSSAAGLVF 570
QY 539 LIAVVVIIVNCNRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDPNEAVREFAK 598
Db 571 VVAVVVIIVNCNRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDPNEAVREFAK 626
QY 599 BIDSCVKIEQVIGAGEFGEVCSGHLKLPKGRIFVAIKTLKSGYTEKQRDFTLSEASIM 658
Db 627 BIDSCVKIEQVIGAGEFGEVCSGHLKLPKGRIFVAIKTLKSGYTEKQRDFTLSEASIM 686
QY 659 QFDPHPNVHLEGVVTKSTPTVMIITEFMENGLSDFLRQNDQFTVITOLVGLMGRGIAAGM 718
Db 687 QFDPHPNVHLEGVVTKSTPTVMIITEFMENGLSDFLRQNDQFTVITOLVGLMGRGIAAGM 746

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QY 719 KYLADMYVHRDLAARNILVNSNLVCKVSDGLSRFLLEDDTSDPTTYSALGKPIRWTA 778
DB KYLSEMYVHRDLAARNILVNSNLVCKVSDGLSRFLLEDDTSDPTTYSALGKPIRWTA 806
QY 779 PEAIQYRKFTSASDWSYGIWMEVMSYGERPYWDMNQDVINAIEDQYRLPPMDPCPSA 838
DB PEAIQYRKFTSASDWSYGIWMEVMSYGERPYWDMNQDVINAIEDQYRLPPMDPCPSA 866
QY 839 LHQLMDCWQRDRNHRPKFGIIVNTLDKMRNPNSLKAAPLSSGGINLPDLRTIPDYS 898
DB LHQLMDCWQRDRNHRPKFGIIVNTLDKMRNPNSLKAAPLSSGGINLPDLRTIPDYS 926
QY 899 FNTVDENLEAKMGYKESFANAGFTSFDDVVSQMMEDILRVGYTLAGHQKILNSIQVM 958
DB FNTVDENLEAKMGYKESFANAGFTSFDDVVSQMMEDILRVGYTLAGHQKILNSIQVM 986
QY 959 RAQMNIQSVQV 970
DB RAQMNIQSVQV 998

RESULT 13

US-08-702-367-20
; Sequence 20, Application US/08702367
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,509
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-367-20

Query Match 71.0%; Score 3632.5; DB 11; Length 998;
Best Local Similarity 70.5%; Pred. No. 1.1e-252;
Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY 4 AVEETLMDSTATAELGMVHPPSGWEEVSGYDENNTITVQVNCVNFSSQNNWLRTPK 63
DB AVEETLMDSTATAELGMVHPPSGWEEVSGYDENNTITVQVNCVNFSSQNNWLRTPK 96
QY 64 IRRRGARRHVMKFSVRDCSSIPSPGCKETFNLYYEADFDSATKTFPNMNPWK 123
DB IRRRGARRHVMKFSVRDCSSIPSPGCKETFNLYYEADFDSATKTFPNMNPWK 156

QY 124 VDTIADESESOVDLGRVMKINTEVSRGVPVSRSGFYLAFOYGGCMGLIAVRFYRKC 183
DB VDTIADESESOVDLGRVMKINTEVSRGVPVSRSGFYLAFOYGGCMGLIAVRFYRKC 212
QY 184 PRIITQNGAIFQETLSGAESTSLVAARGSCITANAEVDVPIKLYCNGDGEWLVPICGMCK 243
DB PRIITQNGAIFQETLSGAESTSLVAARGSCITANAEVDVPIKLYCNGDGEWLVPICGMCK 272
QY 244 AGPFAVENGTVRCPCSGTTPKANOGDEACHTCPINSTRTSEGATNCVCRNGYRADIPL 303
DB AGPFAVENGTVRCPCSGTTPKANOGDEACHTCPINSTRTSEGATNCVCRNGYRADIPL 332
QY 304 DMCPTTIPSAOAVISSVNETSLMLEWTPRDSGRGREDLVYNIICKSC--GSGRGACTRC 361
DB DMCPTTIPSAOAVISSVNETSLMLEWTPRDSGRGREDLVYNIICKSC--GSGRGACTRC 392
QY 362 GDNVQYAPROLGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOAA 421
DB GDNVQYAPROLGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOAA 452
QY 422 PSVSIHMQVSRVDSITLSNSQPDOPNGVILDYELQYEEKELSEYNATAIKSPTNTV-- 479
DB PSVSIHMQVSRVDSITLSNSQPDOPNGVILDYELQYEEKELSEYNATAIKSPTNTV-- 510
QY 480 TGLKAGAIYVQVARTVAGYGRYSGKMYFQMTWE-AEYQTSIQEKLPLIGSSAAGLVF 538
DB TGLKAGAIYVQVARTVAGYGRYSGKMYFQMTWE-AEYQTSIQEKLPLIGSSAAGLVF 570
QY 539 LIAVVIATVNCRRGERADSEYTDKLOHYTSGHIPTGMKIYIDPFTYEDPNEAVREFAK 598
DB LIAVVIATVNCRRGERADSEYTDKLOHYTSGHIPTGMKIYIDPFTYEDPNEAVREFAK 626
QY 599 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKGRIFVAIKTLKSGYTEKQRDRFLSEASIM 658
DB EIDISCVKIEQVIGAGEFGEVCSGHLKLPKGRIFVAIKTLKSGYTEKQRDRFLSEASIM 686
QY 659 GQFDHPNVHLEGVVTKSTPVMILITFEMENGSLDSFLRQNDGQFTVQLVGLRGTAAGM 718
DB GQFDHPNVHLEGVVTKSTPVMILITFEMENGSLDSFLRQNDGQFTVQLVGLRGTAAGM 746
QY 719 KYLADMYVHRDLAARNILVNSNLVCKVSDGLSRFLLEDDTSDPTTYSALGKPIRWTA 778
DB KYLADMYVHRDLAARNILVNSNLVCKVSDGLSRFLLEDDTSDPTTYSALGKPIRWTA 806
QY 779 PEAIQYRKFTSASDWSYGIWMEVMSYGERPYWDMNQDVINAIEDQYRLPPMDPCPSA 838
DB PEAIQYRKFTSASDWSYGIWMEVMSYGERPYWDMNQDVINAIEDQYRLPPMDPCPSA 866
QY 839 LHQLMDCWQRDRNHRPKFGIIVNTLDKMRNPNSLKAAPLSSGGINLPDLRTIPDYS 898
DB LHQLMDCWQRDRNHRPKFGIIVNTLDKMRNPNSLKAAPLSSGGINLPDLRTIPDYS 926
QY 899 FNTVDENLEAKMGYKESFANAGFTSFDDVVSQMMEDILRVGYTLAGHQKILNSIQVM 958
DB FNTVDENLEAKMGYKESFANAGFTSFDDVVSQMMEDILRVGYTLAGHQKILNSIQVM 986
QY 959 RAQMNIQSVQV 970
DB RAQMNIQSVQV 998

RESULT 14

US-09-378-759-20
; Sequence 20, Application US/09378759
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks

STATE: California
 COUNTRY: USA
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/378,759
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/702,367
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Robert B.
 REFERENCE/DOCKET NUMBER: A-287
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 998 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-378-759-20

Query Match 71.0%; Score 3632.5; DB 17; Length 998;
 Best Local Similarity 70.5%; Pred. No. 1.1e-252;
 Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY 4 AVEETLMDSSTTAAELGVMVHPSPGSEVSGYDENMNTIRTYQVCNVPFSSONNMLRTKF 63
 DB 37 ALEETLMDTKWVTSALWTSHPESEVSGYDEAMNPIRTYQVCNVPFSSONNMLRTGF 96

QY 64 IRRGAHRHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFDSATKTFPNMNPWYK 123
 DB 97 IWRDQVRYVELKFTVRDCNSIPNIPGSKETFNLYYEADSDVASASPPFWMNPYK 156

QY 124 VDTIADEFSQVDLGGRYMKINTVRSFGPVSRSFGYLAFOYGGCMSLIAVRYFYK 183
 DB 157 VDTIAPDESFRIDAG---RVNTKVRSGPLSKAGFYLAFOYGGCMSLIAVRYFYK 212

QY 184 PRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGNLPIGRMCK 243
 DB 213 ASTTAGFALPELTGAETSLVIAPICTIPNAVEVSPLKLYCNGDGNLPIGRMCK 272

QY 244 AGFEAVENGTVCRCGSPGTFKAGQDEACTHCPINSRTTSEGATNCVCRNGYIRADLPL 303
 DB 273 TGHEPAKESQCRPCPPGSKAKQGBGCLPCPPNRTTSPAASICTCHNFPYRADS 332

QY 304 DMCPTIPSAQNAVSSVNETSLMELTTPRSGGREDLYVNIICKSC--GSGRGACTRC 361
 DB 333 DSACTVPPSPRGVSNVNETSLILEWSEPRDLGVDRDLYLVNICKHSGAGSACSR 392

QY 362 GDNVYAPRLGTEPRIVISDLAHTQTFEIQAVNGVTDOSPFPQFASVNTITNOAA 421
 DB 393 DNVFVPPQLGSEPRVHTSHLAHRTFFVQAVNGVSGKSPPLPRYAANVITNQAA 452

QY 422 PSASVIMHVSRTVDITLSWQDOPNGVILDEYLOYYEKELESEYNATAIKSPNTV-- 479
 DB 453 PSEVPTLRLHSSSGSLTSLWAPPRNGVILDEYEMKYEK--SEGIASTVTSQMSVOL 510

QY 480 TGLKAGAIYVQVRAKTAVAGYGRSKMYFOIWMTE-AEYQTSQKELPLIIGSSAGLVF 538
 DB 511 DGLRDPARYVQVRAKTAVAGYGRSKMYFOIWMTE-AEYQTSQKELPLIIGSSAGLVF 570

QY 539 LIAVVYAIVCNRRGPERASEYTDRLQHYTSGHIPGKMYIDPTTYPDPNEAVREFAK 598
 DB 571 VVAVVYAIVCNRRGPERASEYTDRLQHYTSGHIPGKMYIDPTTYPDPNEAVREFAK 626

QY 599 EIDISCVKIEQVIGAGEFGEVGRGLKQPGREVEFAIKTLKVGYTEQRORDFLSEASIM 658

DB 627 EIDVSCVKIEVIGAGEFGEVGRGLKQPGREVEFAIKTLKVGYTEQRORDFLSEASIM 686
 QY 659 GQFDHPNVIHLEGVVTSTPMIITEFMENGLSDSLKRONDGQFTVQLVGLMGLGIAAGM 718
 DB 687 GQFDHPNIIIRLEGVVTSTPMIITEFMENGLSDSLKRONDGQFTVQLVGLMGLGIAAGM 746
 QY 719 KYLADMYVHRDLAARNILVNSLVCKVDFGLSFRLEDDTSDPTTYSALGGKPIRWTA 778
 DB 747 KYLSEMYVHRDLAARNILVNSLVCKVDFGLSFRLEDDTSDPTTYSALGGKPIRWTA 806
 QY 779 PEATYRKFTSASDVMSYGVIMVWVMSYGERPYWDMNQOVINAIEQDYRLPPMDPCSA 838
 DB 807 PEATYRKFTSASDVMSYGVIMVWVMSYGERPYWDMNQOVINAIEQDYRLPPMDPCSA 866
 QY 839 LHQMLDCWQRNHRPKFGOIVNTLDKMIKRNPSLKAMAPLSSGINSPLDRIPTDYS 898
 DB 867 LHQMLDCWVRNLRPKFSQIVNTLDKLIIRNAASLKVIASQAQSGMSQPLDRIPTDYS 926
 QY 899 FNTVDLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRVGVTLAGHKKILNSIQVM 958
 DB 927 FTTVGDLDAIKMGYKESFVSAGFASFDLVAQMTAEDLLRIGVTLAGHKKILNSIQVM 986

QY 959 RAQMNQIQSV 970
 DB 987 RLOMNQTLPVQV 998

RESULT 15
 PCT-US01-03800A-2273
 ; Sequence 2273, Application PC/TUS0103800A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-030
 ; CURRENT APPLICATION NUMBER: PCT/US01/03800A
 ; PRIOR FILING DATE: 2001-02-05
 ; PRIOR APPLICATION NUMBER: 09/560,875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 2700
 ; SOFTWARE: Custom
 ; SEQ ID NO 2273
 ; LENGTH: 1007
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 PCT-US01-03800A-2273

Query Match 71.0%; Score 3632.5; DB 1; Length 1007;
 Best Local Similarity 70.5%; Pred. No. 1.1e-252;
 Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY 4 AVEETLMDSSTTAAELGVMVHPSPGSEVSGYDENMNTIRTYQVCNVPFSSONNMLRTKF 63
 DB 46 ALEETLMDTKWVTSALWTSHPESEVSGYDEAMNPIRTYQVCNVPFSSONNMLRTGF 105

QY 64 IRRGAHRHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFDSATKTFPNMNPWYK 123
 DB 106 IWRDQVRYVELKFTVRDCNSIPNIPGSKETFNLYYEADSDVASASPPFWMNPYK 165

QY 124 VDTIADEFSQVDLGGRYMKINTVRSFGPVSRSFGYLAFOYGGCMSLIAVRYFYK 183
 DB 166 VDTIAPDESFRIDAG---RVNTKVRSGPLSKAGFYLAFOYGGCMSLIAVRYFYK 221

QY 184 PRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGNLPIGRMCK 243
 DB 222 ASTTAGFALPELTGAETSLVIAPICTIPNAVEVSPLKLYCNGDGNLPIGRMCK 281

QY 244 AGFEAVENGTVCRCGSPGTFKAGQDEACTHCPINSRTTSEGATNCVCRNGYIRADLPL 303

Db 282 TGHEPAAKESQCRPCPGCYKQKQEGECPLCPPPNSRTTSPAASICTCHNNFYRADSDSA 341
QY 304 DMCCTTIPSAQOAVISSVNETSLMLEWTPRDSGREDLVYNIICKSC--GSGRGACTRC 361
Db 342 DSACTTVSPRGVSNVNETSLILEWSEPRDGLVDLLYNVJCKKCHGAGGASACSRC 401
QY 362 GDNVQYAPROLGLTEPRYIYISDLIAHTQYTFEQAVNGVTDQSPFSQOFASVNTTNOAA 421
Db 402 DDNVFVPRQLGLSEPRVHTSHLLAHTRYTFEQAVNGVSGKSPPLPPRYAAVNTTNOAA 461
QY 422 PSASVIMHQSRTVDSITLSKSPDQPNQVILDYELQYEEKELSEYNATAIKSPTNTV-- 479
Db 462 PSEVPTLRLHSSGSLTSLWAPPENGVILDYEMKYFEK--SEGIASTVTSQMNVSQVL 519
QY 480 TGLKAGAIYVFOVARTVAGYGRYSGKMYQTMTE-AEYQTSIQEKLPLIGSSAAGLVF 538
Db 520 DGLRPDARYVQVARTVAGYQYSPRAEFETTSERGSGAQOEOQLPLVIGSATAGLVF 579
QY 539 LIAVVVIAIVCNRGGERADSEYTDKLQHYTSGHITPGMKIYIDPFTYEDPNEAVREFAK 598
Db 580 WVAVVIAIVCLRQHRGSDSEYTEKLQY----IAPGMVYIDPFTYEDPNEAVREFAK 635
QY 599 EIDISCVKIEQVIGAGEFGEVCGSHLKLPGKREIFVAIKTLKSGYTEKQRDFLSEASIM 658
Db 636 EIDVSCVKEIEVIGAGEFGEVCGRLKQPGRRREVFAIKTLKVGYTEQRDRDFLSEASIM 695
QY 659 GQFDHPNVIHLEGVVTKSTPVMILTEFMENGSLDSFLRNDGQFTVQLVGMRLGTAAGM 718
Db 696 GQFDHPNIIILEGVVTKSRPVMILTEFMENCALDSEFLRNDGQFTVQLVGMRLGTAAGM 755
QY 719 KYLADNMNVYHRDLAARNILVNSNLCKVSDFGLSRFLDDTSDPTVTSALCGKFPPIRWTA 778
Db 756 KYLSENNYVYHRDLAARNILVNSNLCKVSDFGLSRFLDDTSDPTVTSALCGKFPPIRWTA 815
QY 779 PEAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVINAIEDODYRLPPPMDCPSA 838
Db 816 PEAIAYRKFTSASDVWSYGIWMEVMSYGERPYWDMNSQDVINAVEQDYRLPPPMDCPTA 875
QY 839 LHQLMLDCWQKDRNHRPKFGQIYVNTLDKMRNPNSLKMAYPLSSGINLPLDRTIPDYTS 898
Db 876 LHQLMLDCWVRDNRNLRPKFSQIYVNTLDKLIRNAASLKVIASAOSGMSQPLDRTVPDYTT 935
QY 899 FNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMMEDILRVGVTLAGHQKILNSIQVM 958
Db 936 FTTVGDWLDIAIKMGYKESFVSAGFASFDLVAQWTAEDLLRIGVTLAGHQKILSSIQDM 995
QY 959 RAQMNOIQSVEV 970
Db 996 RLQMNOTLPVQV 1007

Search completed: February 1, 2002, 09:59:42
Job time: 402 sec

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